

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 14, 2003, 04:06:46 : Search time 64.5 Seconds

(without alignments)  
8646.160 Million cell updates/sec

Title:

Perfect score: 3490

Sequence:

1 aaagaggaagcagcgtgctc.....ttaactgtctcatccttt 1911

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Fgapop 10.0 , Fgapext 0.5

Delop 6.0 , Delext 7.0

Delop 6.0 , Delext 7.0

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 1083872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DRV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09651150/runat\_12092003\_184345\_9763/app\_query.fasta\_1.2055  
-DB=PublishedApplications\_AA -OFFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosu62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09651150.qcgn.1.1.74.#runat\_12092003\_184345\_9763  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_1/USPTO.spool/US09651150/runat\_12092003\_184345\_9763/app\_query.fasta\_1.2055
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pcp.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pcp.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pcp.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	8.09e-133	2047.00	133	Sequence 2, Appli
2	8.09e-133	2047.00	133	Sequence 683, App
3	8.09e-133	2047.00	133	Sequence 3, Appli
4	8.09e-133	2047.00	133	Sequence 12, Appli
5	8.09e-133	2047.00	133	Sequence 4, Appli
6	8.09e-133	2047.00	133	Sequence 1, Appli
7	8.09e-133	2047.00	133	Sequence 59, Appli
8	8.09e-133	2047.00	133	Sequence 124, App
9	8.09e-133	2047.00	133	Sequence 65, Appli
10	8.09e-133	2047.00	133	Sequence 8, Appli
11	8.09e-133	2047.00	133	Sequence 68, Appli
12	8.09e-133	2047.00	133	Sequence 4, Appli
13	8.09e-133	2047.00	133	Sequence 3, Appli
14	8.09e-133	2047.00	133	Sequence 10, Appli
15	8.09e-133	2047.00	133	Sequence 69, Appli
16	8.09e-133	2047.00	133	Sequence 51, Appli
17	8.09e-133	2047.00	133	Sequence 66, Appli
18	8.09e-133	2047.00	133	Sequence 5, Appli
19	8.09e-133	2047.00	133	Sequence 2, Appli
20	8.09e-133	2047.00	133	Sequence 6, Appli
21	8.09e-133	2047.00	133	Sequence 81, Appli
22	8.09e-133	2047.00	133	Sequence 1, Appli
23	8.09e-133	2047.00	133	Sequence 71, Appli
24	8.09e-133	2047.00	133	Sequence 22, Appli
25	8.09e-133	2047.00	133	Sequence 13, Appli
26	8.09e-133	2047.00	133	Sequence 99, Appli
27	8.09e-133	2047.00	133	Sequence 6, Appli
28	8.09e-133	2047.00	133	Sequence 2, Appli
29	8.09e-133	2047.00	133	Sequence 11093, A
30	8.09e-133	2047.00	133	Sequence 1598, Ap
31	8.09e-133	2047.00	133	Sequence 2, Appli
32	8.09e-133	2047.00	133	Sequence 17, Appli
33	8.09e-133	2047.00	133	Sequence 11739, A
34	8.09e-133	2047.00	133	Sequence 10907, A
35	8.09e-133	2047.00	133	Sequence 2, Appli
36	8.09e-133	2047.00	133	Sequence 14622, A
37	8.09e-133	2047.00	133	Sequence 201, App
38	8.09e-133	2047.00	133	Sequence 250, App
39	8.09e-133	2047.00	133	Sequence 161, App

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Percent Similarity: 99.74% Conservative: 0
Best Local Similarity: 99.74% Mismatches: 1
Query Match: 58.65% Indels: 0
DB: 10 Gaps: 0

US-09-651-150B-1 (1-1911) x US-09-135-239B-2 (1-390)

QY 74 ATGGACTTCCTGGCTTTGGCCACCTTACTTCCTGCCAGTATCAGGGCGCTCAGGATCCTC 133
DB 1 MetAspArgTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu 20

QY 134 CCAGAAGTAAGTAGAGGGAGCTGGCGGATCAGTTACCAATGCAATGCCACTTCCT 193
DB 21 ProGluValLysValGluGlyLeuGlySerValThrIleLysCysProLeuPro 40

QY 194 GAATGCATGTAGGATATATCTGTCGGGAGATGGTGGATCTGGACATGTGCTACC 253
DB 41 GlnLeuHisValArgMetTyrLeuCysArgGlnMetAlaLysProGlyLeuCysSerThr 60

QY 854 GGCCTTTCTCTGGCCTCTCTGGGCTGTGTGAAAGGGCGCTTGAAGGAGGAAA 913
DB 261 GlyLeuPheLeuLeuAlaLeuLeuGlyLeuValValLysArgAlaValGluArgLys 280

QY 914 GGCCTCTCCAGGGCGGGCGGCTGCTGCTGAGGATGCGCGCTCGAGAGTCCGAG 973
DB 281 AlaLeuSerArgAlaArgAlaArgAlaValArgMetArgAlaLeuGluSerSerGln 300

QY 974 AGGCCCCCGGGTGCCTGGAGCCGCTCCCAACACATCTACAGCGCTGCCCGGG 1033
DB 301 ArgProArgGlySerProArgProArgSerGlnAsnIleTyrSerAlaCysProArg 320

QY 1034 CGCGCTCTGGAGCGGAGCTGAGGACACAGGGAGGCGCCCGTTCCTCCGCGCGGAGCG 1093

Db 321 ArgAlaArgGlyAlaAspAlaAlaGlyThrGlyGluAlaProValProGlyProGlyAla 340
QY 1094 CCGTTGGCCCGCCCGCTGAGGTGTCTGAATCTCCCTCCATGCCATGCCATCTGTG 1153
Db 341 ProLeuProAlaProLeuGlnValSerGluSerProTrpLeuHisAlaProSerLeu 360
QY 1154 AAGCCAGCTGTGAATAGCTGAGCTCTACACAGAGCTGCCGCCATGATGAGGACAGT 1213
Db 361 LysThrSerCysGluTyrValSerLeuTyrHisGlnProAlaAlaMetMetGluAspSer 380
QY 1214 GATTTCAGTACTACATCAATGTTCTGCC 1243
Db 381 AspSerAspAspTyrIleAsnValProAla 390

RESULT 2
US-09-866-050A-683
; Sequence 683, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-683

Alignment Scores:
Pred. No.: 6,11e-43 Length: 255
Score: 741.00 Matches: 145
Percent Similarity: 69.65% Conservative: 34
Best Local Similarity: 56.42% Mismatches: 70
Query Match: 21.23% Indels: 8
DB: 11 Gaps: 4

US-09-651-150B-1 (1-1911) x US-09-866-050A-683 (1-255)

QY 74 ATGGACTTCCTGGCTTTGGCCACCTTACTTCCTGCCAGTATCAGGGCGCTCAGGATCCTC 133
DB 1 MetAspArgTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgValLeu 20

QY 134 CCAGAAGTAAGTAGAGGGAGCTGGCGGATCAGTTACCAATGCAATGCCACTTCCT 193
DB 21 ProGluValGlnLeuAsnValGluTrpGlyGlySerIleIleGluCysProLeuPro 40

QY 194 GAATGCATGTAGGATATATCTGTCGGGAGATGGTGGATCTGGACATGTGCTACC 253
DB 41 GlnLeuHisValArgMetTyrLeuCysArgGlnMetAlaLysProGlyLeuCysSerThr 60

QY 254 GTGGTATCCACCACTTCAATCAAGGCAGAAATCAAGGCGCGAGTTACTCTGAAGCAA 313
DB 61 ValValSerAsnThr---PheValLysLysGluTyrGluArgArgValThrLeuThrPro 79

QY 314 TACCCACCAAGAATCTGTCTCTAGTGGAGGTACACAGCTGACAGAAAGTACACGCGGA 373
DB 80 CysLeuAspLysLysLeuPheLeuValGluMetThrGlnLeuThrGluAsnAspGly 99

QY 374 GTCTATGCTCGCGAGCGGGCATGACACAGACCGGGGAAAGACCCAGAAAGTCCACCTG 433
DB 100 IleTyrAlaCysGlyValGlyMetLysThrAspLysGlyLysThrGlnLysIleThrLeu 119

QY 434 AATGTCACAGTGAATAC---GAGCCATCATGGGAGAGCAGCAGCAATGCTGAGACTCCA 490
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Db 120 AsnValHisAsnGluIyProGluProPheTrpGluAspGluTrpIhrSerGluArgPro 139
QY 491 AAATGGTTTCATCTGCCCTATTGTTCCAGATGCCT-----GCATATGCC 535
Db 140 ArgTrpLeuHisArgPheLeuGlnHisGlnMetProTrpLeuHisGlySerGluHisPro 159
QY 536 AGTTCTTCCAAATTCGTAAACAGAGTTACACACAGCTCAAGAGGGCAAGTCCCTCCA 595
Db 160 SerSerSerGlyValIleAlaLysValThrProAlaSerIyThrGluAlaProPro 179
QY 596 GTTCACACATCTCTCCCCACACACCAATCAACCCAGCCCTCGAGTGTCCAGAGCATCT 655
Db 180 ValHisGlnProSerSerIleThrSerValThrGlnHisProArgValTyArgAlaPhe 199
QY 656 TCAGTAGCAGGTGACAGCCCGACACCTTCTGCCATCCACTACAGCTCAAAAATCTCA 715
Db 200 SerValSerAlaThrIySerProAlaLeuLeuProAlaThrAlaSerLysThrSer 219
QY 716 GCTGTGAGGGGTGCTCAAGCCCGACAGCCGCTACACACACACACAGGCTGCAC 775
Db 220 ThrGlnGlnAla---IleArgProLeuGluAlaSerTySerHisHisThrArgLeuHis 238
QY 776 AGCAGACAGCAGTGGACTATGGCTACACTCTGGGAGGGAAGGCCAAGGA 826
Db 239 GluGlnArgThrArgHisHisGlyProHisTyArgArgGluAspArgGly 255
RESULT 3
US-09-135-238B-3
; Sequence 3, Application US/09135238B
; Patent No. US20020177565A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020177565Alan, Garry P.
; APPLICANT: Hitoshi, Yasumichi
; TITLE OF INVENTION: TOSO
; FILE REFERENCE: A65635-1/DJB/RMS
; CURRENT APPLICATION NUMBER: US/09/135,238B
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/066,063
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (13)..(16)
; OTHER INFORMATION: The xaa at positions 13 through 16 represents an
; OTHER INFORMATION: unknown amino acid.
; NAME/KEY: UNSURE
; LOCATION: (44)..(48)
; OTHER INFORMATION: The xaa at positions 44 through 48 represents an
; OTHER INFORMATION: unknown amino acid.
; NAME/KEY: UNSURE
; LOCATION: (61)..(62)
; OTHER INFORMATION: The xaa at positions 61 and 62 represents an
; OTHER INFORMATION: unknown amino acid.
US-09-135-238B-3
Alignment Scores:
Pred. No.: 8.01e-15 Length: 84
Score: 331.50 Matches: 69
Percent Similarity: 84.52% Conservative: 2
Best Local Similarity: 82.14% Mismatches: 2
Query Match: 9.50% Indels: 11
DB: 10 Gaps: 3
US-09-651-150b-1 (1-1911) x US-09-135-238B-3 (1-84)
QY 170 GTTACATCAATGCCACTTCTGAAATGCATGTG-----AGGATATATCTG 217
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Db 1 ValThrIleLysCysProLeuProGluMetHisVal*****ArgIleTyIys 20
QY 218 TCCCGGGAGATGGCTGGATCTGGAACATGTGGIACCGTGGTATCCACACCAACTTCATC 277
Db 21 CysArgGluAsnAlaGlySerGlyThrCysGlyThrValValSerThr***PheIle 40
QY 278 AAGCCAGAA-----TACAAGGGCGGAGTTACTCTCAAGCAATACCCAGC 322
Db 41 LysAlaGlu*****TyriysGlyArgValThrLeuLysGlnTyProArg 60
QY 323 -----AAGAAATCTTCTTAGTGGAGTAACACAGCTGACAGAAAGTGACAGCGAGTC 376
Db 61 *****LysAsnLeuPheLeuValGluValThr***LeuThrGluSerAspSerGlyVal 80
QY 377 TATCCCTGCGGA 388
Db 81 TyrAlaCysGly 84
RESULT 4
US-09-135-238B-12
; Sequence 12, Application US/09135238B
; Patent No. US20020177565A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020177565Alan, Garry P.
; APPLICANT: Hitoshi, Yasumichi
; TITLE OF INVENTION: TOSO
; FILE REFERENCE: A65635-1/DJB/RMS
; CURRENT APPLICATION NUMBER: US/09/135,238B
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/066,063
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 43
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-135-238B-12
Alignment Scores:
Pred. No.: 4.37e-08 Length: 43
Score: 233.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.68% Indels: 0
DB: 10 Gaps: 0
US-09-651-150B-1 (1-1911) x US-09-135-238B-12 (1-43)
QY 971 CAGAGGCGCGGGTCCGCGCGCGCGCTCCCAAAACAACATCTACAGCGCTGCCG 1030
Db 1 GluArgProArgGlySerProArgProArgProArgSerGlnAsnAlaIleTySerAlaCysPro 20
QY 1031 CGCGCGCTCGTGGAGCGGACGCTGACAGGACAGGAGGAGGCCCGTCCGCGCGCGGA 1090
Db 21 ArgArgAlaArgGlyAlaAspAlaAlaGlyThrGlyGluAlaProValProGlyProGly 40
QY 1091 GCGCGCGTGTG 1099
Db 41 AlaProLeu 43
RESULT 5
US-09-950-294-4
; Sequence 4, Application US/09950294
; Patent No. US20020127645A1
; GENERAL INFORMATION:
; APPLICANT: Morrison, Sherie L.
; APPLICANT: Chintalacharuvu, Kote R.
; TITLE OF INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED
; BY SINGLE CELLS AND METHODS FOR MAKING AND USING
; NUMBER OF SEQUENCES: 4
; SAME
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/950,294

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/095,385

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Canady, Karen S

REGISTRATION NUMBER: 39,927

REFERENCE/DOCKET NUMBER: 30435,45USU1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310 445-1140

TELEFAX: 310 445-9031

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 608 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-950-294-4

## Alignment Scores:

Pred. No.:	1,22e-05	Length:	608
Score:	200.00	Matches:	115
Percent Similarity:	35.11%	Conservative:	76
Best Local Similarity:	21.14%	Mismatches:	186
Query Match:	5.73%	Indels:	167
DB:	10	Gaps:	20

US-09-651-150B-1 (1-1911) x US-09-950-294-4 (1-608)

Qy	79	CTTCTGGCTTTGGCCACTTTACTTCCCTGCCAGTATCAGGGGGCCCTGAGGATCCTCCOCAGA	138
Db	6	LeuThrCysLeuLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr	25
Qy	139	AGTAAAGGTAGAGGGGAGTGGGGCGGATCAGTACCAATGCCACTTCCT-----	193
Db	25	oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrProTh	45
Qy	194	-----GAATCATGTGAGGATATATCTGCGCGGAGATGGCTGATGTAACATG	246
Db	45	rSerValAsnArgHisThrArgLysTyrTyrPcysArgGlnGlyAlaArgGlyGly---Cy	64
Qy	247	TGTTACCGTGGTATCCACCACTTCATCAAGCGAGCAATACAGGCGCCGAGTTACTCT	306
Db	64	sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe	84
Qy	307	GAGCAATATCCAGCGAAGATCTGTTCTTAGTGGAGGTACACAGCTGACAGAAAGTGA	366
Db	84	uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs	104
Qy	367	CAGCGAGTCTATGCTCCGCGGAGCGGCATGAACACA-----	403
Db	104	pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValSe	124
Qy	404	-----GACCG	408
Db	124	rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValTyrThrValAspLe	144

Qy	409	GGGAAGACCCAGAAAGTCCACCTGAATGTCCACAGTGAATACGAGCCATCAGGGGAAGA	468
Db	144	uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr	162
Qy	469	GCAGCCAATGCCTGAGACTCCAAAATGGTTTCATCTGCCCTATTGTTCAGATGCCCTGC	528
Db	162	gLysSerLeuTyrIlys-----GlnIleGlyLe	171
Qy	529	ATATGCCAGTTCTT-----CCAAATTCGTAACACAGT	561
Db	171	uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI	191
Qy	562	TACCACACAGCTCAAGGGCAAGTCCCTCCAGTTCCACCATCCCTCCGCCACACCCCA	621
Db	191	leArgLeuAspIleGlnGlyThrGlyGlnLeuPheSerValIleAsnGlnLeuA	211
Qy	622	AATCACCACCGCCCTCGAG-----TGT-----CCAG	648
Db	211	rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspSerAsnSerAsnLysL	231
Qy	649	AGCATCTTCAGTAGCAGGTGACAAAGCCGCAACCTTCCTGCCATCCACTACAGCTCAAA	708
Db	231	ysAsnAlaAspLeuGlnValLeuLysProGlu-LeuValTyrGluAspLeuArg	250
Qy	709	AATCTCAGCTCTGGAGGGCTGTCAAGCCGCCAGCGCC-----	747
Db	251	GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu	270
Qy	748	-----CAGCTACAAACACACACAGGCTGCACAGGAGAGAGACCTGGACTATGGCTC	801
Db	271	CysArgGlnSerSerGlyGluAsnCysAspValValValAsnThrLeuGlyLysArgAla	290
Qy	802	ACAGTCTGGGAGGAAAGGCCAAGGATTTCACATCTCCATCCCGACCATCTGGGCTTTT	861
Db	291	ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe	308
Qy	862	CCTGCTGGCACTTCTGGGCTGGTGTAA-----	891
Db	309	SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis	328
Qy	892	---AAGGGCGTTGAAAGGAGAAAGCCCTCTCCAGCGCGGCCCGCCACTGGCGGTGAG	948
Db	329	SerAspGlyGlnLeuGlnGlySerProIleGlnAlaTrpGlnLeuPheValAsnGlu	348
Qy	949	GATCGCGCCCTGGAGAGTCCACAGAGCCCGCGGGTCCGCGGACGCGGCTCCCAAAA	1008
Db	349	GluSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlySe	365
Qy	1009	CAACATCTACAGCCCTCCCGCGCGGCTCTGGAGCG-----	1048
Db	365	rSerValAlaValLeuCysProTyrAsnArgLysGlnSerLysSerIleLysTyrTrpCy	385
Qy	1049	-----GACGCTGCAGGCACAGGGGCGGCCGCTTCCCGCGCGCGGAGCGCGCTTGCC	1101
Db	385	sLeuTrpGluGlyAlaGlnAsnGlyArg-----	394
Qy	1102	CCCGCGCGCGCTGAGGGTCTGAATCTCCCTGGCTCCATGCCCATCTCTGAACACAG	1161
Db	395	---CysProLeuLeuValAspSerGluGlyTrpValLysAla-----	407
Qy	1162	CTGTGTAATAC-----GTGAGCTCTACACACAGCTGCC-----	1195
Db	408	---GlnTyrGluGlyArgLeuSerLeuGluGluProGlyAsnGlyThrPheThrVa	426
Qy	1195	-----	1195
Db	426	IleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs	446
Qy	1196	-GCCATGATGGAGACAGTATTGATCATCATCAATGTTCTGCTGCTGACACTCCC	1254
Db	446	pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP	462



Db 426 lIleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs 446  
 QY 1196 -GCCATGATGAGGACAGTGAATTCAGATGACTACATCAATGTTCTCGCTGACAACTCC 1254  
 Db 446 pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP 462  
 QY 1255 CAGCTATCCCCAACCCAGGCGGAGCTGTGTGCGCAGGAGTCTCATCTATCTGTGA 1314  
 Db 462 roAsnLeuGlyValProGlyAsnValThrAlaVal-----L 474  
 QY 1315 TGTCCTCAATACCTGCTTCATGTGTTCTCAGAGCCCTCATCACTTCCATGCCCCATCTCGA 1374  
 Db 474 euGlyGluThrLeu-----LysValProCysHisPheProCysLysPheSerS 490  
 QY 1375 CT 1376  
 Db 490 er 490

## RESULT 7

US-09-981-353-59  
 ; Sequence 59, Application US/09981353  
 ; Patent No. US20020160382A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lasek, Amy W.  
 ; APPLICANT: Jones, David A.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
 ; FILE REFERENCE: PA-0038 US  
 ; CURRENT APPLICATION NUMBER: US/09/981,353  
 ; CURRENT FILING DATE: 2001-10-11  
 ; NUMBER OF SEQ ID NOS: 194  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 59  
 ; LENGTH: 764  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20020160382A1 2680109CD1  
 US-09-981-353-59

## Alignment Scores:

Pred. No.: 1,26e-05 Length: 764  
 Score: 200.00 Matches: 115  
 Percent Similarity: 35.11% Conservative: 76  
 Best Local Similarity: 21.14% Mismatches: 186  
 Query Match: 5.73% Indels: 167  
 DB: 10 Gaps: 20

US-09-651-150B-1 (1-1911) x US-09-981-353-59 (1-764)

QY 79 CTCTGGCTTTGGCCACTTACTTCTGCTGAGTATCAGGGGCGCTCAGGATCTCCAG 138  
 Db 6 LeuThrCysLeuLeuAlaPheProAla-IleSerThrLysSerProIlePheGlyPr 25  
 QY 139 ACTAAAGTAGAGGGGAGCTGGCGGATCAGTTACATCAATGCCCCACTTCTCTCT 193  
 Db 25 oGluGluValAsnSerValGluClyAsnSerValSerIleThrCysTyrTrpProIle 45  
 QY 194 -----GAATGCATGTGAGGATATATCTGTCGGGAGATGGCTGGATGGAACATG 246  
 Db 45 rSerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAlaArgGlyGly---Cy 64  
 QY 247 TGGTACCGTGGTATCCACCACCACTTCATCAAGCAGATACACAGGGCGGAGTTACTCT 306  
 Db 64 sIleThrLeuIleSerSerGluGlyThrValSerSerLysThrAlaGlyAlaAsnLe 84  
 QY 307 GAAGCAATACCCACGCAAGAATCTGTCTCTAGTGGAGGTAAACACACTCACAGAAAGTGA 366  
 Db 84 uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs 104  
 QY 367 CAGCGAGTCTATGCTCGGAGCGGGCATGACACA----- 403  
 Db 104 pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValSe 124

QY 404 -----GACCG 408  
 Db 124 rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValThrValAspLe 144  
 QY 409 GGGAAAGACCCAGCAAGTCACTCCCTGAATGTGCCAGTGAATACAGACCATCATGGGAAGA 468  
 Db 144 uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr 162  
 QY 469 GCAGCCAAATGCTGAGACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCCCTGC 528  
 Db 162 gLysSerLeuThrLys-----GlnIleGlyLe 171  
 QY 529 ATATGCCAGTCTCT-----CCAAATCTGTAACACAGT 561  
 Db 171 uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI 191  
 QY 562 TACCACACAGCTCAAGGGGCAAGTCCCTCCAGTTCACACTCTCCGCCACCCACCA 621  
 Db 191 leArgLeuAspIleGlnGlyThrGlnLeuLeuPheSerValIleAsnGlnLeuA 211  
 QY 622 AATCACCACCGCCTCGAG-----TGT-----CCAG 648  
 Db 211 rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspSerAsnSerAsnLysL 231  
 QY 649 AGCATCTTCAGTAGCAGGTGACAAAGCCCGAACCTTCTGCTATCCACTACAGCTCAAA 708  
 Db 231 ysAsnAlaAspLeuGlnValLeuLysProGluProGlu-LeuValTyrGluAspLeuArg 250  
 QY 709 AATCTCAGCTCTGAGGGGCTCTCAAGCCCGCAGAGCC----- 747  
 Db 251 GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu 270  
 QY 748 -----CAGCTACAACCCACACAGGCTGCAGAGCAGAGACTGGACTATGGCTC 801  
 Db 271 CysArgGlnSerSerGlyGluAsnCysAspValValValAsnThrLeuGlyLysArgAla 290  
 QY 802 ACAGTCTGGAGGAGGCGCAAGATTTCATCTCTGATCCGACCATCTCTGGGCCCTTTT 861  
 Db 291 ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe 308  
 QY 862 CCTGCTGGCACTTCTGGGGCTGGTGTGA----- 891  
 Db 309 SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis 328  
 QY 892 ---AAGGGCGCTTGAAGAGGAAAGCCCTCTCAGCGGGCGCGGCGGCTGGCGGTGAG 948  
 Db 329 SerAspGlyGlnLeuGlnGlySerProIleGlnAlaIlePheValAsnGlu 348  
 QY 949 GATGGCGGCGCTGAGAGTCCAGAGGCGCGGGGTGCGCGGCGGCGCTCCCAAAA 1008  
 Db 349 GluSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlySe 365  
 QY 1009 CAACATCTACAGCGCTCCCGCGCGCGCTGTGGAGCG----- 1048  
 Db 365 rSerValAlaValLeuCysProTyrAsnArgLysGluSerLysSerIleLysTyrTrpCy 385  
 QY 1049 -----GAGCTGTCAGGCACAGGGGAGGCGCGCGCTCCCGCGCGCGCGGTGCC 1101  
 Db 385 sLeuTrpGluGlyAlaGlnAsnGlyArg----- 394  
 QY 1102 CCGCGCGCGCTGAGGTGTCTGAATCTCCCTGGTCCATGCCCATCTCTGAAGACCAG 1161  
 Db 395 ---CysProLeuLeuValAspSerGluGlyTrpValLysAla----- 407  
 QY 1162 CTGTGAATAC-----GTGAGCTCTACCCACCGAGCTGCC----- 1195  
 Db 408 ---GlnTyrGluGlyArgLeuSerLeuLeuGluGluProGlyAsnGlyThrPheThrVa 426  
 QY 1195 ----- 1195  
 Db 426 lIleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs 446









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; Patent No. US20020159958A1
; GENERAL INFORMATION:
; APPLICANT: HIAIT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
; TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982.107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-107-4

Alignment Scores:
Pred. No.: 1.48e-05 Length: 746
Score: 199.00 Matches: 113
Percent Similarity: 35.21% Conservative: 75
Best Local Similarity: 21.16% Mismatches: 174
Query Match: 5.70% Indels: 172
DB: Gaps: 22

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QY 215 CTGTGCGGGAGATGGTGGTACATCTGGTACCGGTGATCCACCACTTC 274
D 1111111111111111111111111111111111111111111111111111111
D 37 TrpCysArgGlnGlyAlaArgGlyGly---CysIleThrLeuIleSerSerGluGlyTyr 55
QY 275 ATCAAGCAGCAATACAGGCGCGAGTTACTTGAAGCAATACCCACGCAAGATCTGTC 334
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D 56 ValSerSerLysTyrAlaGlyArgAlaAsnLeuThrAsnPheProGluAsnGlyThrPhe 75
QY 335 CTAGTGGAGGTAAACAGCTCACAGAAAGTACAGCGGAGTCTATGCTGGGAGCGGC 394
D 1111111111111111111111111111111111111111111111111111111
D 76 ValValAsnIleAlaGlnLeuSerGlnAspSerGlyArgTyrLysCysGlyLeuGly 95
QY 395 ATGAACACA-----403
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D 96 IleAsnSerArgGlyLeuSerPheAspValSerLeuGluValSerGlnGlyProGlyLeu 115
QY 404 -----GACGGGGAAGACCCAGAAAGTCACCTGAAT 436
D 1111111111111111111111111111111111111111111111111111111
D 116 LeuAsnAspThrLysValTyrThrValAspLeuGlyArgThr-----ValThrIleAsn 133
QY 437 GTCCACAGTGAATACGACCATCATGGAAGAGAGAGCAATGCTGAGACTCCAAATGG 496
D 1111111111111111111111111111111111111111111111111111111
D 134 CysProPheLysThrGluAsnAlaGlnLysArgLysSerLeuTyrLys-----149
QY 497 TTTCACTGCCCTATTGTTCCAGATGCGCTGCATATGCCAGTTCTT-----542
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D 150 -----GlnIleGlyLeuTyr-ProValLeuValIleAspSerSe 162
QY 543 -----CCAAATTCGTAAACAGAGTTACCACAGCATCAAGGGGCAAGGTC 589
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D 162 rGlyTyrValAsnProAsnTyrThrGlyArgIleArgLeuAspIleGlnGlyThrGlyG 182
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D 182 nLeuLeuPheSerValValIleAsnGlnLeuArgLeuSerAspAlaGlyGlnTyrLeuCy 202
QY 644 T-----CCAGAGCATCTTTCAGTAGCAGGTGACAGGCC 676
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Db 202 sGlnAlaGlyAspAspSerAsnSerAsnLysLysAsnAlaAspLeuGlnValLeuLysPr 222
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QY 737 CCCAGAGGCC-----CAGCTACACACACACACACAGG 769
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D 242 lYProGluValAlaAsnValAlaLysPheLeuCysArgGlnSerSerGlyGluAsnCysA 262
QY 770 CTGCACAGCAGAGAGCAGTGCATATGCTGCACAGTCTGGGAGGAGGCCAAGATT 829
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D 262 spValValAsnThrLeuGlyLysArgAlaProAlaPheGlnGlyArgIleLeuLeuA 282
QY 830 CACATCTCTGATCCGCGCATCCGCTGCTGCTGCGCTGCTGCGGCTGGGTG 889
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D 282 snProGlnAspLysasp-----GlySerPheSerValIleThrGlyLeuArgLysG 300
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D 300 luAspAlaGlyArgTyrLeuCysGlyAlaHisSerAspGlyGlnLeuGlnGlySerP 320
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D 337 erProThrValVal-LysGlyValAlaGlySerSerValAlaValLeuCysProTyrAsn 356
QY 1037 GCTCGTGGAGCG-----GAGCGTGCAGGCACAGGGAG 1069
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D 357 ArgLysGluSerLysSerIleLysTyrTrpCysLeuTrpGluGlyAlaGlnAsnGlyArg 376
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D 377 -----CysProLeuLeuValAspSerGlu 384
QY 1130 CCTGTGCTCCATGCCCTCTCTGAAGACCACTGCTGAATAC-----GTGAGCCTC 1180
D 1111111111111111111111111111111111111111111111111111111
D 385 GlyTrpValLysAla-----GlnTyrGlnGlyArgLeuSerLeu 397
QY 1181 TACCACACGCTGCC-----1195
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D 398 LeuGluGluProGlyAsnGlyThrPheThrValIleLeuAsnGlnLeuThrSerArgAsp 417
QY 1196 -----GCCATGATGGAGGACAGTGCATGCAT 1222
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D 418 AlaGlyPheTyrTrpCysLeuThrAsnGlyAspThrLeu-TrpArgThrThrValGluI 437
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D 437 eLys-----IleIleGluGlyGluProAsnLeuLysValProGlyAsnValTh 453
QY 1283 TGTGTGCCAAGAGTCTCATCTATCTGCTGATGTCATATACCTCTTCATGTTGTTCTCA 1342
D 1111111111111111111111111111111111111111111111111111111
D 453 lAlaVal-----LeuGlyGluThrLeu-----Ly 461
QY 1343 GAGCCCTCATCATCTCCATGCCATGCCATCTCGACT 1376
D 1111111111111111111111111111111111111111111111111111111
D 461 sValProCysHisPheProCysLysPheSerSer 472

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## RESULT 13

US-09-818-247-4

; Sequence 4, Application US/09818247

; Patent No. US20020102657A1

; GENERAL INFORMATION:

; APPLICANT: Mostov, Keith E.

; APPLICANT: Chapin, Steven J.

; APPLICANT: Richman-Eisenstat, Janice

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component

; TITLE OF INVENTION: No. US20020102657A1-Stalk Region of p1gr and Methods of Use T

FILE REFERENCE: 18062E-000910US  
CURRENT APPLICATION NUMBER: US/09/818,247  
CURRENT FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: WO PCT/US01/09699  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 60/192,197  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 60/192,198  
PRIOR FILING DATE: 2000-03-27  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 771  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: mouse polymeric immunoglobulin receptor (pIgR)  
US-09-818-247-4

Alignment Scores:  
Pred. No.: 2,04e-05 Length: 771  
Score: 197.00 Matches: 50  
Percent Similarity: 48.63% Conservative: 21  
Best Local Similarity: 34.25% Mismatches: 59  
Query Match: 5.64% Indels: 16  
DB: 10 Gaps: 4

US-09-651-150B-1 (1-1911) x US-09-818-247-4 (1-771)

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QY 140 GTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAATGCCCACCTCCIGAA--- 196  
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QY 197 -----ATGCAATGAGGATATATCTGTGCGGGAGATGGCTGGATCTGGAACATGT 247  
Db 46 SerValAsnArgHisThrArgLysTyrTrpCysArgGlnGlyAla---SerGlyMetCys 64  
QY 248 GGTACCGGTGATCCACCACCACTTCATCAAGGAGCAATACAGGGCCGAGTTACTCTG 307  
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QY 308 AAGCAATACCCACCAAGAACTCTTCTAGTGGAGGTAAACACAGCTCAGCAAAAGTAC 367  
Db 85 IleAsnPheProGluAsnAsnThrPheValIleAsnIleGluGlnLeuThrGlnAspAsp 104  
QY 368 AGCGAGTCTATGCTGCGGAGCGGCATGAACACAGACCGGGGAAAGACCCAGAAAGTC 427  
Db 105 ThrGlySerTyrLysCysGlyLeuGly---ThrSerAsnArgGlyLeuSerPheAspVal 123  
QY 428 ACCCTGAATGTCACAGTAATACAGGCCATCATGGGAGAGCAGCCAAATGCTCGAGACT 487  
Db 124 SerLeuGluVal-----SerGlnValProGluLeu 133  
QY 488 CCAAAATGGTTTCATCTG 505  
Db 134 ProSerAspThrHisVal 139

RESULT 14

US-09-818-247-3  
Sequence 3, Application US/09818247  
Patent No. US20020102657A1  
GENERAL INFORMATION:  
APPLICANT: Mostov, Keith E.  
APPLICANT: Chapin, Steven J.  
APPLICANT: Richman-Eisenstat, Janice  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,  
TITLE OF INVENTION: No. US20020102657A1-Stalk Region of pIgR and Methods of Use Ther  
FILE REFERENCE: 18062E-000910US

CURRENT APPLICATION NUMBER: US/09/818,247  
CURRENT FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: WO PCT/US01/09699  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 60/192,197  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 60/192,198  
PRIOR FILING DATE: 2000-03-27  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 769  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:  
OTHER INFORMATION: rat polymeric immunoglobulin receptor (pIgR)  
US-09-818-247-3

Alignment Scores:  
Pred. No.: 0.000116 Length: 769  
Score: 186.00 Matches: 53  
Percent Similarity: 49.69% Conservative: 28  
Best Local Similarity: 32.52% Mismatches: 51  
Query Match: 5.33% Indels: 31  
DB: 10 Gaps: 7

US-09-651-150B-1 (1-1911) x US-09-818-247-3 (1-769)

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Db 17 SerThrGlnSerPro-----IlePheGlyProGlnAsp-ValSerSerIleGlu----- 32  
QY 151 GGGGGAGCTGGCGGATCAGTTACCATCAAAATGCCCACTTCTCTGAA-----At 198  
Db 33 -----GlyAsnSerValSerIleThrCysTyrTyrProAspIhrSerValAsnAr 49  
QY 199 GCATGTGAGATATATCTGTGCCGGAGATGGCTGGATCTGGACATGTGTGACGTGGT 258  
Db 49 gHisThrArgLysTyrTrpCysArgGlnGlyAla---AsnGlyTyrCysAlaThrLeuL 68  
QY 259 ATCCACCACCACTTCATCAAGGCAGATACAGGGCCGAGTACTCTGAACAAATACCC 318  
Db 68 eSerSerAsnGlyTyrLeuSerLysGluIhrSerGlyArgAlaSerLeuIleAsnPhePr 88  
QY 319 AGCGAAGATCTGTTCTTAGTGGAGTACACAGCTGACAGAAAGTGACAGCGGAGTCTA 378  
Db 88 cgluAsnSerThrPheValIleAsnIleAlaHisLeuThrGlnGluAspThrGlySerTy 108  
QY 379 TGCCTGCGGAGCGGCATGAACACACACCGGGGAAAGACCCAGAGAGTCCACCTGAATGT 438  
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QY 439 CCACAGTGAATACAGAGCCATCATGGGAGAGCAGCAATGCTGAGACTCCAAATGGT 498  
Db 127 l-----SerGlnValProGluPheProAsnAspTh 137  
QY 499 TCATCTGT 505  
Db 137 rHisVal 139

RESULT 15

US-09-982-107-10  
Sequence 10, Application US/09982107  
Patent No. US20020159958A1  
GENERAL INFORMATION:  
APPLICANT: HIATT, ANDREW C.  
APPLICANT: HEIN, MICHAEL B.  
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING  
TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE

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; FILE REFERENCE: EPI3002E
; CURRENT APPLICATION NUMBER: US/09/982,107
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-982-107-10

Alignment Scores:
Pred. No.:      0.000116      Length:      769
Score:          186.00      Matches:      53
Percent Similarity: 49.69%      Conservative: 28
Best Local Similarity: 32.52%      Mismatches: 51
Query Match:      5.33%      Indels:      31
DB:              10      Gaps:      7

US-09-651-150B-1 (1-1911) x US-09-982-107-10 (1-769)

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4 SerLeuPheAlaLeuValThrValPheSer-----GlyVal 16

QY 91 CCCACTTTACTTCCTGCCAGTATCAGGGGCCCTCAGGATCCTCCAGAGTAAGGTAGA 150
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
17 SerThrGlnSerPro-----IlePheGlyProGlnAsp-ValSerSerIleGlu----- 32

QY 151 GGGGAGGTGGGGGATCAGTTACCATCAATGCCACTTCTGTGAA-----AT 198
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33 -----GlyAsnSerValSerIleThrCysTyrTyrProAspThrSerValAsnAr 49

QY 199 GCATGTGAGGATATATCTGCCGGAGATGGCTGGATCTGGACATCTGGTACCGTGGT 258
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
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QY 259 ATCCACCACCAACTTCATCAGGCAGATACAGGGCCGAGTTACTCTGAAGCAATACCC 318
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
68 eSerSerAsnGlyTyrLeuSerLysGluTyrSerGlyArgAlaSerLeuIleAsnPhePr 88

QY 319 ACACAAGAAATCTGTCTAGTGGAGTAACACAGCTGACAGAAAGTGACAGCGAGTCTA 378
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
88 oGluAsnSerThrPheValIleAsnIleAlaHisLeuThrGlnGluAspThrGlySerTy 108

QY 379 TGCCTGGCGGCGGCATGACACAGACCGGGGAAAGACCCAGAAAGTCACCCCTGAATGT 438
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
108 rLysCysGlyLeuGly---ThrThrAsnArgGlyLeuPheAspValSerLeuGluVa 127

QY 439 CCACAGTGAATACGAGCCATCATGGGAAGACGAGCAATGCTGAGACTCCGAAATGGTT 498
Db 11111 11111 11111 11111 11111 11111 11111 11111 11111 11111
127 l-----SerGlnValProGluPheProAsnAspTh 137

QY 499 TCATCTG 505
Db 11111
137 rHisVal 139
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Job time : 91.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 14, 2003, 02:14:10 ; Search time 24 Seconds

(without alignments)  
6738.004 Million cell updates/sec

Title: US-09-651-150B-1

Perfect score: 3490

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2056	58.9	390	3	US-08-961-564A-2
2	2047	58.7	390	4	US-09-050-861B-2
3	1194.5	34.2	422	4	US-09-724-864-45
4	559	16.0	107	3	US-08-961-564A-4
5	380	10.9	73	4	US-09-050-861B-3
6	233	6.7	43	4	US-09-050-861B-12
7	200	5.7	608	4	US-09-095-385-4
8	200	5.7	771	3	US-08-434-000A-8
9	200	5.7	771	4	US-09-312-157-8
10	199	5.7	746	3	US-08-434-000A-4
11	199	5.7	746	4	US-09-312-157-4
12	187	5.4	109	3	US-08-961-564A-9

13	186	5.3	769	3	US-08-434-000A-10	Sequence 10, Appl
14	186	5.3	769	4	US-09-312-157-10	Sequence 10, Appl
15	182	5.2	757	3	US-08-434-000A-6	Sequence 6, Appli
16	182	5.2	757	4	US-09-312-157-6	Sequence 6, Appli
17	180.5	5.2	1184	4	US-09-266-225D-18	Sequence 18, Appl
18	178	5.1	1185	3	US-09-041-886-23	Sequence 23, Appl
19	167.5	4.8	624	2	US-08-642-408A-22	Sequence 22, Appl
20	167.5	4.8	624	4	US-09-199-534-22	Sequence 22, Appl
21	167.5	4.8	624	4	US-09-199-534-22	Sequence 22, Appl
22	167.5	4.8	773	3	US-08-434-000A-2	Sequence 2, Appli
23	167.5	4.8	773	4	US-09-312-157-2	Sequence 2, Appli
24	164.5	4.7	589	4	US-09-252-991A-28836	Sequence 28836, A
25	158.5	4.5	657	4	US-09-252-991A-28001	Sequence 28001, A
26	158	4.5	1298	2	US-08-690-473-2	Sequence 2, Appli
27	158	4.5	1298	3	US-09-259-821A-2	Sequence 2, Appli
28	158	4.5	1298	3	US-08-843-659-2	Sequence 2, Appli
29	156.5	4.5	726	4	US-09-252-991A-20675	Sequence 20675, A
30	150.5	4.3	407	4	US-09-252-991A-31517	Sequence 31517, A
31	150.5	4.3	500	4	US-09-252-991A-19739	Sequence 19739, A
32	150	4.3	328	4	US-09-252-991A-21969	Sequence 21969, A
33	148.5	4.3	351	4	US-09-252-991A-18476	Sequence 18476, A
34	148	4.2	774	4	US-09-252-991A-16789	Sequence 16789, A
35	147.5	4.2	826	4	US-09-894-998A-47	Sequence 24254, A
36	147.5	4.2	826	4	US-09-894-998A-47	Sequence 24254, A
37	146	4.2	355	3	US-08-483-533-41	Sequence 47, Appl
38	146	4.2	355	4	US-09-283-471A-41	Sequence 41, Appl
39	146	4.2	355	5	FCI-US91-06532-3	Sequence 3, Appli
40	146	4.2	638	4	US-09-252-991A-27068	Sequence 27068, A
41	146	4.2	663	4	US-09-252-991A-30843	Sequence 30843, A
42	145	4.2	538	4	US-09-252-991A-32064	Sequence 32064, A
43	144.5	4.1	1520	4	US-09-252-991A-17501	Sequence 17501, A
44	144	4.1	478	4	US-09-252-991A-25191	Sequence 25191, A
45	143.5	4.1	616	4	US-09-252-991A-25638	Sequence 25638, A

#### ALIGNMENTS

#### RESULT 1

US-08-961-564A-2  
; Sequence 2, Application US/08961564A  
; Patent No. 6114515  
; GENERAL INFORMATION:  
; APPLICANT: WU, SHUJIAN  
; APPLICANT: SWEET, RAYMOND  
; APPLICANT: TRUNEL, ALEMSEGED  
; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN  
; TITLE OF INVENTION: GENE SUPERFAMILY  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,564A  
; FILING DATE: 30-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,935  
; FILING DATE: 25-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70236  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 390 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-564A-2

Alignment Scores:  
Pred. No.: 2,3e-168 Length: 390  
Score: 2056.00 Matches: 390  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 58.91% Indels: 0  
DB: 3 Gaps: 0

US-09-651-150B-1 (1-1911) x US-08-961-564A-2 (1-390)

QY 74 ATGGACTTCTGGCTTGGCCACTTCTTCTGCGGAGATGGCTGGATCTGGACATCTGGTACC 133  
DB 1 MetAspPheTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu 20  
QY 134 CCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTACCATCAATGCCCACCTTCT 193  
DB 21 ProGluValLysValGluGlyLeuGlyGlySerValThrIleLysCysProLeuPro 40  
QY 194 GAAATGCATGACAGATATCTGTCGGGAGATGGCTGGATCTGGACATCTGGTACC 253  
DB 41 GluMetHisValArgIleTyrLeuCysArgGluMetAlaGlySerGlyThrCysGlyThr 60  
QY 254 GTGGTATCCACACCACTTTCATCAAGCAGCAATAAAGGGCCGAGTTACTCTGAAGCAA 313  
DB 61 ValValSerThrThrAsnPheIleLysAlaGluTyrLysGlyArgValThrLeuLysGln 80  
QY 314 TACCCACGAGAATCTGTTCTAGTGAGGTAAACACAGCTCAGAGAAAGTCACAGCGGA 373  
DB 81 TyrProArgLysAsnLeuPheLeuValGluValThrGlnLeuThrGluSerAspSerGly 100  
QY 374 GTCTATGCTGGGAGCGGGCATGAACACAGACCGGGGAAAGACCCAGAAAGTCACCCG 433  
DB 101 ValTyrAlaCysGlyAlaGlyMetAsnThrAspArgGlyLysThrGlnLysValThrLeu 120  
QY 434 AATGTCCACAGTGAATACAGCCATCATGGGAGAGCAGCCCAATGCCTGAGACTCCAAA 493  
DB 121 AsnValHisSerGluTyrGluProSerTrpGluGluGlnProMetProgluThrProLys 140  
QY 494 TGGTTTCATCTCCCTATTTGTTCCAGATGCCGTGATATGCCAGTTCTTCCAAATTCGTA 553  
DB 141 TrpPheHisLeuProTyrLeuPheGlnMetProAlaTyrAlaSerSerLysPheVal 160  
QY 554 ACCAGAGTTACACACCACTCAAGGGGCAAGGTCCTTCCAGTTCCACCACTCTCCCTCCC 613  
DB 161 ThrArgValThrThrProAlaGlnArgGlyLysValProProValHisHisSerPro 180  
QY 614 ACCACCCAAATCACCACCGCTCGAGTGTCCAGAGCATCTTCAGTAGCAGGTGACAG 673  
DB 181 ThrThrGlnIleThrHisArgProArgValSerArgAlaSerSerValAlaGlyAspLys 200  
QY 674 CCCGAACTTCTGCTCCACTACAGCTCAAAAATCTCAAAAATCTGAGCTGGAGGGCTG 733  
DB 201 ProArgThrPheLeuProSerThrThrAlaSerLysIleSerAlaLeuGluGlyLeuLeu 220  
QY 734 AAGCCCCAGACGCCAGCTTACACCAACCAAGCTGCACAGGCGAGAGCAGTGGAC 793  
DB 221 LysProGlnThrProSerTyrAsnHisHisThrArgLeuHisArgGlnArgAlaLeuAsp 240  
QY 794 TATGGTCACTCTGGGAGGAGAGCCCAAGGATTTTCATCTGATCCCGACCATCTCG 853  
DB 241 TyrGlySerGlnSerGlyArgGluGlyGlnGlyPheHisIleLeuIleProThrIleLeu 260

QY 854 GGCCTTTTCTCTGCTGCACCTTCTGGGCTGGTGGTGAAGAAGCGCCGTGAAAGAGGAAA 913  
DB 261 GlyLeuPheLeuLeuAlaLeuLeuGlyLeuValValLysArgAlaValAlaGluArgLys 280  
QY 914 GCCCTCTCCAGCGGGCCCGGACTGGCCGTGAGGATCGCGCCCTGGAGAGCTCCCAAG 973  
DB 281 AlaLeuSerArgAlaArgLeuAlaValArgMetArgAlaLeuGluSerSerGln 300  
QY 974 AGGCCCCGGGCTCGCGCGCTCCCAAAACACATCTACAGCCCTGCGCGCGG 1033  
DB 301 ArgProArgGlySerProArgProArgSerGlnAsnAsnIleTyrSerAlaCysProArg 320  
QY 1034 CGCGCTCTGGAGCGAGCTGCAGGCACAGGGAGGCCCCGTTCCCGCCCGGAGCG 1093  
DB 321 ArgAlaArgGlyAlaAspAlaAlaGlyThrGlyGluAlaProValProGlyProGlyAla 340  
QY 1094 CGTTTGGCCCCCGCGCTGCAGGTGTCTGAATCTCCCTGGCTCCATCCCATCTCTG 1153  
DB 341 ProLeuProAlaProLeuGlnValSerGluSerProTrpLeuHisAlaProSerLeu 360  
QY 1154 AAGACCAGCTGTGAATPACGTGAGCCCTTACCACCGCTGCGCGCCATGATGGAGGACAT 1213  
DB 361 LysThrSerCysGluTyrValSerLeuTyrHisGlnProAlaAlaMetMetGluAspSer 380  
QY 1214 GATTTCAGATGACTACATCAATCTCTCTGCC 1243  
DB 381 AspSerAspAspIleAsnValProAla 390

## RESULT 2

US-09-050-861B-2  
Sequence 2, Application US/09050861B  
Patent No. 6553314  
GENERAL INFORMATION:  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING  
FILE REFERENCE: RIGL-002CON  
CURRENT APPLICATION NUMBER: US/09/050,861B  
CURRENT FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: US/09/651,150B  
PRIOR FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: US 09/050,861  
PRIOR FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 390  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-050-861B-2

Alignment Scores:  
Pred. No.: 1,37e-167 Length: 390  
Score: 2047.00 Matches: 389  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 58.65% Indels: 0  
DB: 4 Gaps: 0

US-09-651-150B-1 (1-1911) x US-09-050-861B-2 (1-390)

QY 74 ATGGACTTCTGGCTTGGCCACTTCTTCTGCGGAGATGGCTGGATCTGGACATCTGGTACC 133  
DB 1 MetAspPheTrpLeuTrpProLeuTyrPheLeuProValSerGlyAlaLeuArgIleLeu 20  
QY 134 CCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTACCATCAATGCCCACCTTCT 193  
DB 21 ProGluValLysValGluGlyGluLeuGlyGlySerValThrIleLysCysProLeuPro 40  
QY 194 GAAATGCATGAGGATATCTGTCGGGAGATGGCTGGATCTGGACATCTGGTACC 253  
DB 41 GluMetHisValArgIleTyrLeuCysArgGluMetAlaGlySerGlyThrCysGlyThr 60  
QY 254 GTGGTATCCACCACTTTCATCAAGGCGAGAAATCAAGGGCGGAGTTACTCTGAAGCAA 313

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Db 61 ValValSerThrThrAsnPhelIleLysAlaGluTyrLysGlyArgValThrLeuLysGln 80
QY 314 TACCCACGCAAGATCTGTCTAGTGGAGGTAAACAGCTGACAGAAAGTACAGCGGA 373
Db 81 TyrProArgLysAsnLeuPheLeuValGluValThrGlnLeuThrGluSerAspSerGly 100
QY 374 GTCTATCGCTCGGAGCGGGCATGAACACAGACCGGGGAAGACCCAGAAAGTACCCCTG 433
Db 101 ValTyrAlaCysGlyAlaGlyMetAsnThrAspArgGlyLysThrGlnLysValThrLeu 120
QY 434 AATGTCACAGTGAATACGAGCCATCATGGGAAGACAGCAATGCTGAGACTCCAAAA 493
Db 121 AsnValHisSerGluTyrGluProSerTrpGluGluProMetProGluThrProLys 140
QY 494 TGGTTTCATCTGCCCTATTGTTCAGATGCCCTGCATATGCCAGTCTTCCCAATTCGTA 553
Db 141 TrpPheHisLeuProTyrLeuPheGlnMetProAlaTyrAlaSerSerLysPheVal 160
QY 554 ACCAGAGTTACACACAGCTCAAGGGGCAAGTCCCTCCAGTTCACCACTCTCCCTCC 613
Db 161 ThrArgValThrThrProAlaGlnArgGlyLysValProProValHisSerSerPro 180
QY 614 ACACCCAAATCACCCACCGCCCTCGAGTGTCCAGAGCATCTTCAGTAGCAGGTGACAAG 673
Db 181 ThrThrGlnIleThrHisArgProArgValSerArgAlaSerSerValAlaGlyAspLys 200
QY 674 CCGCAAGACTCTCGCANTCCACTACAGCTCAAAAATCTCAGCTCTGAGGGGCTGCTC 733
Db 201 ProArgThrPheLeuProSerThrThrAlaSerLysIleSerAlaLeuGluGlyLeuLeu 220
QY 734 AAGCCCCAGACGCCAGCTACACACACACAGCTGCACAGGCTGCACAGGACAGACAGCAG 793
Db 221 LysProGlnThrProSerTyrAsnHisThrArgLeuHisArgGlnArgAlaLeuAsp 240
QY 794 TATGGCTCACAGTCTGGAGGAAGCCCAAGGATTCACATCTGATCCGACCATCCCTG 853
Db 241 TyrGlySerGlnSerGlyArgGluGlyGlnGlyPheHisIleLeuIleProThrIleLeu 260
QY 854 GGCCTTTCTCTGCTGCTGCTGCTGGCTGGTGGTGAAGAGGCGCTTGAAGAGGAGAA 913
Db 261 GlyLeuPheLeuLeuAlaLeuLeuGlyLeuValValLysArgAlaValGluArgArgLys 280
QY 914 GGCCTCTCCAGCGGGCGCGGCTGAGGCTGAGGATCGCGCGCTGAGAGCTCCGAG 973
Db 281 AlaLeuSerArgArgAlaArgArgLeuAlaValArgMetArgAlaLeuGluSerSerGln 300
QY 974 AGSGCCCGGGTCCGCGGACCGGCTCCCAAAACACATCTACAGCGCTGCGCGCGG 1033
Db 301 ArgProArgGlySerProArgProArgSerGlnAsnAsnIleTyrSerAlaCysProArg 320
QY 1034 CGCGCTCTGAGCGGAGCTGACGACAGGAGGAGGCGCGCTTCCGCTCCATGCCCATCTCTG 1093
Db 321 ArgAlaArgGlyAlaAspAlaGlyThrGlyGluAlaProValProGlyProGlyAla 340
QY 1094 CGGTGCGCGCGCGCGCTGAGGTGTGAATCTCCCTGCTCCATGCCCATCTCTG 1153
Db 341 ProLeuProAlaProLeuGlnValSerGluSerProTrpLeuHisAlaProSerLeu 360
QY 1154 AAGACCACTGTGATAGTGTGAGCTCTACACAGCGCTGCGCGCTGATGAGGAGACAGT 1213
Db 361 LysThrSerCysGluTyrValSerLeuTyrHisGlnProAlaAlaMetMetGluAspSer 380
QY 1214 GATTCAGATGACTACATCAATCTTCTCTGCC 1243
Db 381 AspSerAspAspTyrIleAsnValProAla 390
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## RESULT 3

```
US-09-724-864-45
; Sequence 45, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
```

```
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Mouse
; US-09-724-864-45
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## Alignment Scores:

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Pred. No.: 2,41e-94 Length: 422
Score: 1194.50 Matches: 243
Percent Similarity: 68.32% Conservative: 46
Best Local Similarity: 57.45% Mismatches: 113
Query Match: 34.23% Indels: 21
DB: 4 Gaps: 7
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US-09-651-150B-1 (1-1911) x US-09-724-864-45 (1-422)
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QY 74 ATGGACTTGTGGCTTTGGCCACTTACTTCTCCAGTATCAGGGGCCCTGAGGATCCTC 133
Db 1 MetAspPheTrpLeuLeuTyrPheLeuProValSerGlyAlaLeuArgValLeu 20
QY 134 CCAGAAGTAAAGTAGAGGGGAGCTGGCGGGATGATGATGATGATGATGATGATGATG 193
Db 21 ProGluValGlnLeuAsnValGluTrpGlyGlySerIleIleIleGluCysProLeuPro 40
QY 194 GAAATCAATGTAGGATATATCTGTGCGGGAGATGGCTGGATCTCGAACATGTGTGATC 253
Db 41 GlnLeuHisValArgMetTyrLeuCysArgGlnMetAlaLysProGlyIleCysSerThr 60
QY 254 GTGGTATCCACCACCACTTCATCAAGGCAGATACAGGGCCGAGTTCCTCTGTAAGCAA 313
Db 61 ValValSerAsnThr---PheValLysLysGluTyrGluArgValThrLeuThrPro 79
QY 314 TACCCACGCAAGATCTGTCTAGTGGAGGTAAACAGCTGACAGAAAGTACAGCGGA 373
Db 80 CysLeuAspLysLysLeuPheLeuValGluMetThrGlnLeuThrGluAsnAspGly 99
QY 374 GTCTATCGCTCGGAGCGGGCATGAACACAGACCGGGGAAGACCCAGAAAGTACCCCTG 433
Db 100 IleTyrAlaCysGlyValGlyMetLysThrAspLysGlyLysThrGlnLysIleThrLeu 119
QY 434 AATGTCACAGTGAATAC---GAGCCATCATGGGAAGACAGCAATGCTGAGACTCCA 490
Db 120 AsnValHisGlnProSerIleThrSerValThrGlnHisProArgValTyrArgAlaPhe 199
QY 491 AATGTTTCATCTGCCCTATTGTTCAGATGCCCT---GCAATATGCC 553
Db 140 ArgTrpLeuHisArgPheLeuGlnHisGlnMetProTrpLeuHisGlySerGluHisPro 159
QY 536 AGTTCTTCCAAATTCGTAAACAGAGTTACACACAGCTCAAGAGGCGGCGCTCCCTCCA 595
Db 160 SerSerSerGlyValIleAlaLysValThrThrProAlaSerLysThrGluAlaProPro 179
QY 596 GTTCACCACTCTCTCCCGCCACCCCAATATCACCCCGCGCTGAGTGTCCAGAGCATCT 655
Db 180 ValHisGlnProSerSerIleThrSerValThrGlnHisProArgValTyrArgAlaPhe 199
QY 656 TCAGTAGCAGGTGACAAAGCCCGCAACCTTCTCCGCTCCACTACAGCTCAAAATCTCA 715
Db 200 SerValSerAlaThrLysSerProAlaLeuLeuProAlaThrThrAlaSerLysThrSer 219
QY 716 GCTCTGGAGGGCTGCTCAAGCCCGCAGAGCGCCAGCTACACACACACAGGCTGAC 775
Db 220 ThrGlnGlnAla---IleArgProLeuGluAlaSerTyrSerHisThrArgLeuHis 238
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Score: 380.00 Matches: 72  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 98.63% Mismatches: 0  
 Query Match: 10.89% Indels: 0  
 DB: 4 Gaps: 0

US-09-651-150B-1 (1-191) x US-09-050-861B-3 (1-73)

QY 170 GTTACATCAATGCCACTTCTCGAATGATGAGGATATATCTGTGCGGGAGATG 229  
 Db 1 ValThrIleLysCysProLeuProGluMetHisValArgIleLysLeuCysArgGluMet 20  
 QY 230 GCTGATCGAAGATGGTACCGTGTATCCACCACTTCATCAAGGCAATAC 289  
 Db 21 AlaGlySerGlyThrCysGlyThrValValSerThrAsnPheIleLysAlaGluTrp 40  
 QY 290 AAGGCCGAGTACTCTCAAGCAATACCCAGCAGATCTGTCTAGTGAGTAACA 349  
 Db 41 LysGlyArgValThrLeuLysGlnTyrProArgLysAsnLeuPheValGluValThr 60  
 QY 350 CAGCTGACAGAAAGTGACAGCGGAGTCTATCGCTGCGGA 388  
 Db 61 GlnLeuThrGluSerAspSerGlyValTyrAlaCysGly 73

# RESULT 6

US-09-050-861B-12  
 ; Sequence 12, Application US/09050861B  
 ; Patent No. 6555314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payan, Donald  
 ; TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING  
 ; FILE REFERENCE: RIGL-002CON  
 ; CURRENT APPLICATION NUMBER: US/09/050.861B  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: US/09/651,150B  
 ; PRIOR FILING DATE: 2000-08-30  
 ; PRIOR APPLICATION NUMBER: US 09/050,861  
 ; PRIOR FILING DATE: 1998-03-30  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 43  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-050-861B-12

## Alignment Scores:

Pred. No.: 3,75e-12 Length: 43  
 Score: 233.00 Matches: 43  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 6.68% Indels: 0  
 DB: 4 Gaps: 0

US-09-651-150B-1 (1-191) x US-09-050-861B-12 (1-43)

QY 971 CAGAGCGCGGGTGGCGGCGGACCGGCTCCCAAAACATCTACAGCGCTGCCG 1030  
 Db 1 GlnArgProArgGlySerProArgProArgSerGlnAsnIleTyrSerAlaCysPro 20  
 QY 1031 CGCGCGCTGTCGAGCGACGCTGACGACAGGAGGAGGCGCCCGTTCGCCGCCGGA 1090  
 Db 21 ArgArgAlaArgGlyAlaAspAlaAlaGlyThrGlyAlaProValProGlyProGly 40  
 QY 1091 GCSCCGTTG 1099  
 Db 41 AlaProLeu 43

# RESULT 7

US-09-095-385-4  
 ; Sequence 4, Application US/09095385  
 ; Patent No. 6300104  
 ; GENERAL INFORMATION:

APPLICANT: Morrison, Sherie L.  
 APPLICANT: Chintalachu, Kote R.  
 TITLE OF INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED  
 BY SINGLE CELLS AND METHODS FOR MAKING AND USING  
 TITLE OF INVENTION: SAME  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
 STREET: 11150 Santa Monica Boulevard, Suite 400  
 CITY: Los Angeles  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 90025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/095.385  
 FILING DATE: 09-JUN-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/050,969  
 FILING DATE: 19-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Canady, Karen S  
 REGISTRATION NUMBER: 39,927  
 REFERENCE/DOCKET NUMBER: 30435.45USU1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310 445-1140  
 TELEFAX: 310 445-9031  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 608 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-095-385-4

## Alignment Scores:

Pred. No.: 7,52e-09 Length: 608  
 Score: 200.00 Matches: 115  
 Percent Similarity: 35.11% Conservative: 76  
 Best Local Similarity: 21.14% Mismatches: 186  
 Query Match: 5.73% Indels: 167  
 DB: 4 Gaps: 20

US-09-651-150B-1 (1-191) x US-09-095-385-4 (1-608)

QY 79 CTTCTGCTTTGGCCACTTTACTTCTGCGGAGTATGAGGCGCCCTGAGATCTCCAG 138  
 Db 6 LeuThrCysLeuLeuAlaValPheProAla-IleSerThrLysSerProIlePheGlyPr 25  
 QY 139 AGTAAAGTAGAGGGAGCTGGCGGATCAGTATACCATCAATGCGCCACTTCTCT 193  
 Db 25 oGluGluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrProTh 45  
 QY 194 -----GAAATGCATGTAGGATATATCTGCGGAGATGCTGGATCTGGAACATG 246  
 Db 45 rSerValAsnArgHisThrArgLysTyrIrpCysArgGlnGlyAlaArgGlyGly---Cy 64  
 QY 247 TGGTACCGTGGTATCCACCACCACTTCATCAAGGCAAGATACAAAGGCGGAGTTACTCT 306  
 Db 64 sIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArgAlaAsnLe 84  
 QY 307 GAAGCAATACCCACGCAAGAAATCTGTCTCTAGTGGAGGTAAACAGCTGACAGAAAGTGA 366  
 Db 84 uThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSerGlnAspAs 104  
 QY 367 CAGCGGAGTCTATGCTGCGGAGCGGATGAACACA----- 403

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Db 104 pSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerArgGlyLeuSerPheAspValse 124
Qy 404 -----GACCG 408
Db 124 rLeuGluValSerGlnGlyProGlyLeuLeuAsnAspThrLysValTyrThrValAspLe 144
Qy 409 GGGAAAGACCCAGAAAGTCAACCTGAATGTCCACAGTGAATACAGAGCCATCATGGGAAGA 468
Db 144 uGlyArgThr-----ValThrIleAsnCysProPheLysThrGluAsnAlaGlnLysAr 162
Qy 469 GCAGCCAAATCGCTGAGACTCCAAAATGGTTTCATCTCCCTATTTGTTCCAGATGCTGC 528
Db 162 gLysSerLeuTyrLys-----GlnIleGlyLe 171
Qy 529 ATATGCCAGTTCIT-----CCAAATTCGTAACACAGAGT 561
Db 171 uTyr-ProValLeuValIleAspSerSerGlyTyrValAsnProAsnTyrThrGlyArgI 191
Qy 562 TACCACACACAGCTCAAAAGGGCAAGTCCCTCCAGTTCACCACTCCCTCCGCCACCAACCA 621
Db 191 leArgLeuAspIleGlnGlyThrGlyGlnLeuLeuPheSerValValIleAsnGlnLeuA 211
Qy 622 AATCACCACCGCTCGAG-----TGT-----CCAG 648
Db 211 rgLeuSerAspAlaGlyGlnTyrLeuCysGlnAlaGlyAspAspSerAsnLysL 231
Qy 649 AGCATCTTCACTAGCAGTCAAGCCCGACAGCTCTCTGCCATCCATCCAGCTCAAA 708
Db 231 ysAsnAlaAspLeuGlnValLeuLysProGluProGlu-LeuValTyrGluAspLeuArg 250
Qy 709 AATCTCAGCTCTGGAGGGCTGTCAAGCCGCCAGCGCC----- 747
Db 251 GlySerValThrPheHisCysAlaLeuGlyProGluValAlaAsnValAlaLysPheLeu 270
Qy 748 -----CAGCTACACACACACAGCTCCAGGAGCAGAGCAGTGGACTATGGCTC 801
Db 271 CysArgGlnSerSerGlyGluAsnCysAspValValValAsnThrLeuGlyLysArgAla 290
Qy 802 ACAGTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
Db 291 ProAlaPheGluGlyArgIleLeuLeuAsnProGlnAspLysAsp-----GlySerPhe 308
Qy 862 CTGCTGCATCTCTGGGGCTGGTGTGAA----- 891
Db 309 SerValValIleThrGlyLeuArgLysGluAspAlaGlyArgTyrLeuCysGlyAlaHis 328
Qy 892 ---AAGGCCCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 948
Db 329 SerAspGlyGlnLeuGlnGlySerProIleGlnAlaTrpGlnLeuPheValAsnGlu 348
Qy 949 GATGCGCGCTGGAGAGCTCCAGAGGCGCGCGGCTCGCGCGCGCGCTCCCAAAA 1008
Db 349 GluSer-----ThrIleProArgSerProThrValVal-LysGlyValAlaGlyse 365
Qy 1009 CAACATCTACAGCGCTCGCGCGCGCGCTCGCGCGCGCTCGCGCGCGCTCGCGCGCTCGCG 1048
Db 365 rSerValAlaValLeuCysProTyrAsnArgLysGluSerLysSerIleLysTyrTrpCy 385
Qy 1049 -----CAGCTGCAGGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1101
Db 385 sLeuTrpGluGlyAlaGlnAsnGlyArg----- 394
Qy 1102 CCCCAGCGCTGAGGAGTGTGTAATCTCCCTGGCTCCATGCGCCCATCTCTCAAGACCAAG 1161
Db 395 ---CysProLeuLeuValAspSerGluGlyTrpValLysAla----- 407
Qy 1162 CTGTGAATAC-----GTGAGCTCTACACACAGCTGCC----- 1195
Db 408 ---GlnTyrGluGlyArgLeuSerLeuLeuGluGluProGlyAsnGlyThrPheThrVa 426
Qy 1195 ----- 1195
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Db 426 lIleLeuAsnGlnLeuThrSerArgAspAlaGlyPheTyrTrpCysLeuThrAsnGlyAs 446
Qy 1196 -GCCATGATGAGGACACACTGATTCAGATGACTATCATCAATGTTCTCTGCTGACACACTCCC 1254
Db 446 pThrLeu-TrpArgThrThrValGluIleLys-----IleIleGluGlyGluP 462
Qy 1255 CAGCTATCCCCACACCCAGCTCGGACTGTGTGGTGGCAAGGAGTCTCATCTATCTGCTGA 1314
Db 462 roAsnLeuLysValProGlyAsnValThrAlaVal-----L 474
Qy 1315 TGTCCATACCTGCTTCATGTGTCTCAGAGCCCTCATCTCCCATGCCCCCATCTGGA 1374
Db 474 euGlyGluThrLeu-----LysValProCysHisPheProCysLysPheSerS 490
Qy 1375 CT 1376
Db 490 er 490

RESULT 8
US-08-434-000A-8
; Sequence 8, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIAIT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 1
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; DESCRIPTION: Mouse Polymunoglobulin Receptor
US-08-434-000A-8

Alignment Scores: 8.28e-09 Length: 771
Pred. No.: 200.00 Matches: 55
Score: 44.57% Conservative: 23
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FILING DATE: <Unknown>

APPLICANT: K.-C. MA, THOMAS LEHNER  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/434,000A

FILING DATE:  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application  
 PRIOR APPLICATION DATA: described below: 1

APPLICATION NUMBER: 08/367,395  
 FILING DATE: 12/30/94

ATTORNEY/AGENT INFORMATION:  
 NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613  
 REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159  
 TELEX: 67-3510

SEQUENCE LISTING  
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 746 amino acids

TYPE: amino acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 DESCRIPTION: Human Polymunoglobulin Receptor

US-08-434-000A-4

#### Alignment Scores:

Pred. No.: 9,96e-09 Length: 746  
 Score: 199.00 Matches: 113  
 Percent Similarity: 35.21% Conservative: 75  
 Best Local Similarity: 21.16% Mismatches: 174  
 Query Match: 5.70% Indels: 172  
 DB: 22 Gaps: 22

US-09-651-150B-1 (1-1911) x US-08-434-000A-4 (1-746)

QY	107	CCAGTATCAGGGCCCTCAGGATCTCCAGAGTAAGTAGAGGGGAGCTGGCGGA	166
DB	3	ProfilePheGly-----ProGlu---GluValAsnSerValGluGlyAsn	16
QY	167	TCAGTTACCATCAATGCCACTTCCT-----GAAATCATGTGAGGATATAT	214
DB	17	SerValSerIleThrCysTyrTyrProProThrSerValAsnArgHisThrArgLysTyr	36
QY	215	CTGTCCGGGAGATCGTGGATCTGGAACATGTGTACCGTGTATCCACCAACTTC	274
DB	37	TrpCysArgGlnGlyAlaArgGlyGly---CysIleThrLeuIleSerSerGluGlyTyr	55
QY	275	ATCAAGGAGCAATCAAGGGCCAGTTACTCTGAAGCAATACCCACGCAAGAAATCTGTTTC	334
DB	56	ValSerSerLysTyrAlaGlyArgAlaAsnLeuThrAsnPheProGluAsnGlyThrPhe	75
QY	335	CTAGTGGAGGTAAACAGCTGACAGAAAGTGAACCGGAGTCTATGCTCGGAGCGGGC	394
DB	76	ValValAsnIleAlaGlnLeuSerGlnAspSerGlyArgTyrLysCysGlyLeuGly	95

QY	395	ATGAACACA-----	403
DB	96	IleAsnSerArgGlyLeuSerPheAspValSerLeuGluValSerGlnGlyProGlyLeu	115
QY	404	-----GACCGGGGAAAGACCCAGAAAGTCACCCCTGAAT	436
DB	116	LeuAsnAspThrLysValTyrThrValAspLeuGlyArgThr-----ValThrIleAsn	133
QY	437	GTCCACAGTGAATACGACCATCATGGGAGAGCAGCAATGCCTGAGACTCCAAAATGG	496
DB	134	CysProPheLysThrGluAsnAlaGlnLysArgLysSerLeuTyrLys-----	149
QY	497	TTTCATCTGCCCTATTTCCTCCAGATGCCTGCATATGCCAGTCTT-----	542
DB	150	-----GlnIleGlyLeuTyr-ProValLeuValIleAspSerSe	162
QY	543	-----CCAAATTCGTACACAGAGTACACACACAGCTCAAGGGGCAAGGTC	589
DB	162	rGlyTyrValAsnProAsnTyrThrGlyArgIleArgLeuAspIleGlnGlyThrGlyG1	182
QY	590	CCTCAGTTCACCACTCCTCCCCACCAACCAATCACCACCGCCCTCGAG-----TG	643
DB	182	nLeuLeuPheSerValValIleAsnGlnLeuArgLeuSerAspAlaGlyGlnTyrLeuCy	202
QY	644	T-----CCAGAGCATCTTCAGTAGCAGGTCAACAGGCC	676
DB	202	sglnAlaGlyAspAspSerAsnSerAsnLysLysAsnAlaAspLeuGlnValLeuLysPr	222
QY	677	CGAACCTTCCTGCCATCCACTACAGCCTCAAAATCTCAGCTCTGGAGGGCTGCTCAAG	736
DB	222	oGluProGlu-LeuValTyrGluAspLeuArgGlySerValThrPheHisCysAlaLeuG	242
QY	737	CCCCAGAGGCC-----CAGCTACACCAACCAACCAACCCAGG	769
DB	242	lyProGluValAlaAsnValAlaLysPheLeuCysArgGlnSerSerGlyGluAsnCysA	262
QY	770	CTGCACAGCAGAGACACTGGACTATGCCTCACAGTCTGGGAGGAGGCCAAGATT	829
DB	262	spValValValAsnThrLeuGlyLysArgAlaProAlaPheGluGlyArgIleLeuLeuA	282
QY	830	CACATCTCTGATCCCGACCATCCTGGGCCTTTCTCTGCTGGCACTTCTGGGGCTGGTGG	889
DB	282	snProGlnAspLysAsp-----GlySerPheSerValValIleThrGlyLeuArgLysG	300
QY	890	AA-----AAGGCCGTTGAAAGAGGAAGCC	916
DB	300	IuAspAlaGlyArgTyrTyrLeuCysGlyAlaHisSerAspGlyGlnLeuGlnGlySerP	320
QY	917	CTCTCAGCGCGGGCCCGCGACTGGCGGTGAGGATGCGCGCTGGAGAGCTCCAGAGG	976
DB	320	roileGluAlaTrpGlnLeuPheValAsnGluGluSer-----ThrIleProArgS	337
QY	977	CCCCCGGGTCCCGCGCGCTCCCAACACATCTACAGCGCTGCCCGCGCGCGCC	1036
DB	337	erProThrValVal-LysGlyValAlaGlySerSerValAlaValLeuCysProTyrAsn	356
QY	1037	GCTCTGGAGCG-----GACGTCGAGGCACAGGGAG	1069
DB	357	ArgLysGluSerLysSerIleLysTyrTrpCysLysLeuTrpGluGlyAlaGlnAsnGlyArg	376
QY	1070	GCCCCCGTTCGCCGGCCCGGCGCGTTCGCCCGCCCGCTGCAGGTGCTGAATCT	1129
DB	377	-----CysProLeuLeuValAspSerGlu	384
QY	1130	CCCTGGCTCCATGCCCATCTCTGAAGACCACTGTGTGATAC-----GTGAGCCCTC	1180
DB	385	GlyTyrValLysAla-----GlnTyrGluGlyArgLeuSerLeu	397
QY	1181	TACCACACGCTGCC-----	1195
DB	398	LeuGluGluProGlyAsnGlyThrPheThrValIleLeuAsnGlnLeuThrSerArgAsp	417
QY	1196	-----GCCATGATGAGGACAGTGTATCAGAT	1222

Db 418 AlaGlyPheTyrTrpCysLeuThrAsnGlyAspThrLeu-TpArgIhrThrValGluI 437  
 QY 1223 GACTACATCAATGTCCTGACAACTCCCGACGTAATCCCGACCGGTCGGAC 1282  
 Db 437 eLys-----IleIleGluGlyGluProAsnLeuLysValProGlyAsnValTh 453  
 QY 1283 TGTGTGTCAGGAGTCTCACTATCTGCTGATGTCACAAATACCTGCTTCAITGTTCTCA 1342  
 Db 453 rAlaVal-----LeuGlyGluThrLeu-----Ly 461  
 QY 1343 GAGCCCTCATCTCCATCCCGCCCATCTCGACT 1376  
 Db 461 sValProCysHisPheProCysLysPheSerSer 472

RESULT 11

US-09-312-157-4  
 ; Sequence 4, Application US/09312157  
 ; Patent No. 6303341  
 ; GENERAL INFORMATION:  
 ; APPLICANT: K.-C. MA, THOMAS LEHNER  
 ; K.-C. MA, THOMAS LEHNER  
 ; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
 ; PROTEINS IN PLANTS AND THEIR USES  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/312,157  
 ; FILING DATE: 14-May-1999  
 ; CLASSIFICATION DATA:  
 ; APPLICATION NUMBER: 08/434,000  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Guise, Jeffrey W.  
 ; REGISTRATION NUMBER: 34,613  
 ; REFERENCE/DOCKET NUMBER: 212/127  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 552-8400  
 ; TELEFAX: (619) 552-0159  
 ; TELEX: 67-351  
 ; SEQUENCE LISTING  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 746 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; DESCRIPTION: Human Polymunoglobulin Receptor  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4

Alignment Scores:  
 Pred. No.: 9,96e-09 Length: 746  
 Score: 199.00 Matches: 113  
 Percent Similarity: 35.21% Conservative: 75  
 Best Local Similarity: 21.16% Mismatches: 174  
 Query Match: 5.70% Indels: 172  
 DB: 4 Gaps: 22

US-09-651-150b-1 (1-1911) x US-09-312-157-4 (1-746)  
 QY 107 CCAGTATCAGGGCCCTGAGGATCTCCAGCAAGTAAGGTAGAGGGGAGCTGGCGGA 166  
 Db 3 ProIlePheGly-----ProGlu---GluValAsnSerValGluGlyAsn 16  
 QY 167 TCAGTTACATCAAAATGCGCCACTTCCT-----GAAATGCATGTGAGGATATAT 214  
 Db 17 SerValSerIleThrCysTyrTyrProProThrSerValAsnArgHisThrArgLysIyr 36  
 QY 215 CTGTCCGGGAGATGCTGGAATCTGCAATCTGTACGGTGTACGGTGTATCCACCAACATCTC 274  
 Db 37 TrpCysArgGlnGlyAlaArgGlyGly---CysIleThrLeuIleSerSerGluGlyTyr 55  
 QY 275 ATCAAGCGAGATAACAGGGCGGAGTTACTCTTGAAGCAATACCCGCAAGAATCTGTTC 334  
 Db 56 ValSerSerLysTyrAlaClyArgAlaAsnLeuThrAsnPheProGluAsnGlyThrPhe 75  
 QY 335 CTAGTGGAGTAACACAGCTGACAGAAAGTGCACGGGAGTCTATGCTCGGGAGCGGC 394  
 Db 76 ValValAsnIleAlaGlnLeuSerGlnAspSerGlyArgLysCysGlyLeuGly 95  
 QY 395 ATGAACACA----- 403  
 Db 96 IleAsnSerArgGlyLeuSerPheAspValSerLeuGluValSerGlnGlyProGlyLeu 115  
 QY 404 -----GACCGGGAAAGACCCAGAAAGTCAACCTGCTGCTT----- 542  
 Db 116 LeuAsnAspThrLysValTyrThrValAspLeuGlyArgThr-----ValThrIleAsn 133  
 QY 437 GTCCACAGTGAATACGAGCCCATCATGGGAAGAGAGCAATGCTCGGAGACTCCAAATGG 496  
 Db 134 CysProPheLysThrGluAsnAlaGlnLysArgLysSerLeuTyrLys----- 149  
 QY 497 TTTCATCTGCCCTATTGTTCCAGATGCTCATGCTGCTGCTT----- 542  
 Db 150 -----GlnIleGlyLeuTyr-ProValIleValIleAspSerSe 162  
 QY 543 -----CCAAATCGTAACAGAGTACCACACAGCTCAAGGCGGCAAGGTC 589  
 Db 162 rGlyTyrValAsnProAsnTyrThrGlyArgIleArgLeuAspIleGlnGlyThrGlyG1 182  
 QY 590 CTTCCAGTTCACCACTCTCTCCCGACCAATATCCACCGCCCTCGAG-----TG 643  
 Db 182 nLeuPhePheSerValValIleAsnGlnLeuArgLeuSerAspAlaGlyGlnIyrLeuCy 202  
 QY 644 T-----CCAGAGCATCTTCAGTAGCAGGTGACAAAGCC 676  
 Db 202 sGlnAlaGlyAspAspSerAsnSerAsnLysLysAsnAlaAspLeuGlnValLeuLysPr 222  
 QY 677 CGAACCTTCTGCTGCTACAGCTCAAAATCTCAGCTCTGAGGGGCTGCTCAAG 736  
 Db 222 oGluProGlu-LeuValTyrGluAspLeuArgLysSerValThrPheHisCysAlaLeuG 242  
 QY 737 CCCAGAGCGC-----CAGCTACACACCAACACACAGG 769  
 Db 242 lyProGluValAlaAsnValAlaLysPheLeuCysArgGlnSerSerGlyLeuAsnCysA 262  
 QY 770 CTGCACAGGAGAGACACTGGACTATGGCTCACAGCTCGGAGGAGGCAAGGATTT 829  
 Db 262 spValValValAsnThrLeuGlyLysArgAlaProAlaPheGluGlyArgIleLeuLeuA 282  
 QY 830 CACATCTGATCCGACCATCTCTGGGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889  
 Db 282 snProGlnAspLysAsp-----GlySerPheValValIleThrGlyLeuArgLysG 300  
 QY 890 AA-----AAGGCGCGTTGAAGAGAGAGAGCC 916  
 Db 300 luAspAlaGlyArgTyrLeuCysGlyAlaHisSerAspGlyGlnLeuGlnGluGlySerP 320  
 QY 917 CTCTCCAGGCGGCGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 976  
 Db 320 rolleGlnAlaTrpGlnLeuPheValAsnGluGluSer-----ThrIleProArgS 337

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;
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-564A-9
;
; Alignment Scores:
; Pred. NO.: 4.89e-08 Length: 109
; Score: 187.00 Matches: 41
; Percent Similarity: 56.07% Conservative: 19
; Best Local Similarity: 38.32% Mismatches: 41
; Query Match: 5.36% Indels: 6
; DB: 3 Gaps: 3
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; US-09-651-150B-1 (1-191) x US-08-961-564A-9 (1-109)
;
; QY 134 CCAGAAGTAAAGTAGAGGGGAGCTGGCGGATCAGTTACCATCAAAATGCCACTTCCT 193
; DB 4 ProGlu---GluValAsnSerValGluGlyAsnSerValSerIleThrCysTyrTyrPro 22
;
; QY 194 -----GAAATGCATGTGAGGATATATCTGTCGCCGGAGATG---GCTGGATCT 238
; DB 23 ProThrSerValAsnArgHisThrArgLysTyrTrpCysArgGlnProGlyAlaArgGly 42
;
; QY 239 GGAACATGTGTACCGTGTATCCACCAACCACTTCATCAAGGGCAGATAAGGGCGCA 298
; DB 43 GlyLeuCysIleThrLeuIleSerSerGluGlyTyrValSerSerLysTyrAlaGlyArg 62
;
; QY 299 GTTACTCTGCAAGCAATACCCACGCAAGAAATCTGTTCTCTAGTGGAGGTAAACAGCTGACA 358
; DB 53 AlaAsnLeuThrAsnPheProGluAsnGlyThrPheValValAsnIleAlaGlnLeuSer 82
;
; QY 359 GAAAGTGACAGCGGAGTCTATGCTGCGGAGGGGCGATGACACACAGACCGGGGAGAGACC 418
; DB 83 GlnAspAspSerGlyArgTyrLysCysGlyLeuGlyIleAsnSerLeuArgGlyLeuSer 102
;
; QY 419 CAGAAAGTCACCTGCAATGTC 439
; DB 103 PheAspValSerLeuGluVal 109
;
; RESULT 13
; US-08-434-000A-10
; Sequence 10, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
;
; QY 977 CCGCGGGTCCGCGACCGCTCCCAAAACACATCTACAGCGCTCCGCGGCGC 1036
; DB 337 erProThrValVal-LysGlyValAlaGlySerSerValAlaValLeuCysProTyrAsn 356
;
; QY 1037 GCTCGTGGAGCG-----GACGCTGCGAGCAGCAGGGGAG 1069
; DB 357 ArgLysGluSerLysSerIleLysTyrTrpCysLeuTrpGluGlyAlaGlnAsnGlyArg 376
;
; QY 1070 GCCCGCGTCCGCGCGCGGAGCGCGCTTCCCGCGCGCGCTGCGAGGTGCTGGAATCT 1129
; DB 377 -----CysProLeuLeuValAspSerGlu 384
;
; QY 1130 CCTGGCTCCATGCCCATCTCTGAGACAGCTGTGAATAC-----GTGAGCGCTC 1180
; DB 385 GlyTrpValLysAla-----GlnTyrGluGlyArgLeuSerLeu 397
;
; QY 1181 TACCACAGCGCTGCC-----Ly 1195
; DB 398 LeuGluGluProGlyAsnGlyThrPheThrValIleLeuAsnGlnLeuThrSerArgAsp 417
;
; QY 1196 -----GCCATGATGGAGGACAGTGATTCAGAT 1222
; DB 418 AlaGlyPheTyrTrpCysLeuThrAsnGlyAspThrLeu-TrpArgThrThrValGluIle 437
;
; QY 1223 GACTATACATCAATGTTCTGCTGACAACTCCCGAGCTATCCCGCAACCCAGGCTCGGAC 1282
; DB 437 eLys-----IleIleGluGlyGluProAsnLeuLysValProGlyAsnValTh 453
;
; QY 1283 TGTGGTGCCAGGAGTCTCATCTATCTGCTGATGTCGAATACCGCTTCATGTTCTWCA 1342
; DB 453 rAlaVal-----LeuGlyGluThrLeu-----Ly 461
;
; QY 1343 GAGCGCTCATCACTTCCATGCCCGCCCATCTCGACT 1376
; DB 461 svalProCysHisPheProCysLysPheSerSer 472
;
; RESULT 12
; US-08-961-564A-9
; Sequence 9, Application US/08961564A
; Patent No. 6114515
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMESEGED
; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,564A
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,935
; FILING DATE: 25-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700

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Db 68 eSerSerAsnGlyTyrLeuSerLysGlyTyrSerGlyArgAlaSerLeuLeuAsnPhePr 88
QY 319 ACCCAAGAATCTCTCTAGTGGAGTAAACACAGCTGACAGAAAGTACAGCGGAGTCTA 378
Db 88 oGluAsnSerThrPheValIleAsnIleAlaHisLeuThrGlnGluAspThrGlySerTy 108
QY 379 TGCTCGGGAGCGGATGACACAGACCGGGGAAAGACCCAGAAAGTACACCTGATGT 438
Db 108 rLysCysGlyLeuGly---ThrThrAsnArgGlyLeuPhePheAspValSerLeuGluVa 127
QY 439 CCACAGTGAATACAGCCATCATGGGAAGAGCAGCCAAATGCCGACACCTCAAAATGGTT 498
Db 127 l-----SergInValProGluPheProAsnAspTh 137
QY 499 TCATCTG 505
Db 137 rHisVal 139
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## RESULT 15

US-08-434-000A-6

; Sequence 6, Application US/08434000A

; Patent No. 6046037

## GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,000A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application 1

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/367,395

; FILING DATE: 12/30/94

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 757 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; DESCRIPTION: Bovine Polyimmunoglobulin Receptor

US-08-434-000A-6

Alignment Scores:

Pred. No.: 2.89e-07

Score: 182.00

Length: 757

Matches: 42

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Percent Similarity: 51.22% Conservative: 21
Best Local Similarity: 34.15% Mismatches: 44
Query Match: 5.21% Indels: 16
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QY 161 -----GGCGATCAGTTACCATCAATGCCCACCTCTCT-----GAAATG 199
Db 30 SerValGluGlyArgSerValSerIleLysCysTyrTyrProProThrSerValAsnArg 49
QY 200 CATGTGAGGATATATCTGTGCGGGAGATGGCTGGAATCTGGAACATGTGTACCGTGTA 259
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QY 260 TCCACCACCACTTCATCAAGGAGCAATACAAAGGGCGAGTACTCTGAGCAATACCCA 319
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QY 320 CGCAAGAATCTGTTCTTAGTGGAGTAACACAGCTGACAGAAAGTGACAGCGAGTCTAT 379
Db 89 GluSerGlyThrPheValValAspIleSerHisLeuThrHisLysAspSerGlyArgTyr 108
QY 380 GCCTGCGGAGCGGCATGACACAGACCGGGGAAAGACCCAGAAAGTACACCTGAAATGC 439
Db 109 LysCysGlyLeuGlyIleSerSer---ArgGlyLeuAsnPheAspValSerLeuGluVal 127
QY 440 CACAGTGA 448
Db 128 SerGlnAsp 130
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Search completed: September 14, 2003, 04:07:46

Job time : 46 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2003, 23:38:04 ; Search time 124 Seconds  
(without alignments)  
6802.284 Million cell updates/sec

Title: US-09-651-150B-1

Perfect score: 1911

Sequence: 1 aaaggagtaagcagcgtgctc.....ttactctgtctcattcttt 1911

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 11139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1911	100.0	1911	4	US-09-050-861B-1
2	1842.4	96.4	2040	3	US-08-961-564A-1
3	676	35.4	1047	3	US-08-961-564A-3
4	563.6	29.5	1480	4	US-09-724-864-11
5	56.2	2.9	7218	1	US-08-232-463-14
6	48.2	2.5	2430	4	US-09-232-160-16
7	43.4	2.3	7218	1	US-08-232-463-14
8	41.8	2.2	1433	2	US-08-666-392A-1
9	41.8	2.2	1433	3	US-09-199-926-1
10	40.8	2.1	152331	3	US-09-128-155-16
11	40.6	2.1	7812	3	US-09-368-590-1
12	39.2	2.1	636	4	US-09-252-991A-1441
13	39.2	2.1	1131	4	US-09-252-991A-1675
14	39.2	2.1	1671	4	US-09-252-991A-1539
15	38.4	2.0	1920	4	US-09-160-496-4
16	37.6	2.0	1984	4	US-08-937-067-5
17	37	1.9	429	4	US-09-252-991A-15260
18	37	1.9	750	4	US-09-252-991A-15355
19	37	1.9	1386	4	US-09-252-991A-15331
20	37	1.9	1461	4	US-09-252-991A-15308
21	36.6	1.9	618	4	US-09-252-991A-7654
22	36.6	1.9	936	4	US-09-416-509C-2
23	36.6	1.9	1515	1	US-08-221-750A-4
24	36.6	1.9	2571	4	US-09-984-880-1
25	36.6	1.9	7742	1	US-08-221-750A-1
26	36.6	1.9	20966	4	US-09-984-880-3
27	36.4	1.9	672	4	US-09-565-808-3

28	36.4	1.9	1044	1	US-07-975-526-3	Sequence 3, Appli
29	36.4	1.9	1044	4	US-07-974-409C-425	Sequence 425, App
30	36.4	1.9	1929	5	PCT-US93-00031-18	Sequence 18, Appl
31	36.4	1.9	1932	5	PCT-US93-00031-20	Sequence 20, Appl
32	36.4	1.9	1935	4	US-09-620-312D-236	Sequence 236, App
33	36.4	1.9	1941	5	PCT-US93-00031-10	Sequence 10, Appl
34	36.4	1.9	1941	5	PCT-US93-00031-22	Sequence 22, Appl
35	36.4	1.9	2205	5	PCT-US93-00031-12	Sequence 12, Appl
36	36.4	1.9	2208	5	PCT-US93-00031-14	Sequence 14, Appl
37	36.4	1.9	2217	5	PCT-US93-00031-8	Sequence 8, Appl
38	36.4	1.9	2220	5	PCT-US93-00031-16	Sequence 16, Appl
39	36.4	1.9	2811	4	US-08-482-073-3	Sequence 3, Appl
40	36.4	1.9	2813	2	US-08-344-155C-99	Sequence 99, Appl
41	36.4	1.9	2813	4	US-09-009-490A-90	Sequence 90, Appl
42	36.4	1.9	3080	4	US-08-482-073-4	Sequence 4, Appl
43	36.4	1.9	3332	4	US-09-423-890-11	Sequence 11, Appl
44	36.2	1.9	990	4	US-09-252-991A-1499	Sequence 1499, Ap
45	36.2	1.9	1260	4	US-09-252-991A-13265	Sequence 13265, A

## ALIGNMENTS

RESULT 1

US-09-050-861B-1

; Sequence 1, Application US/09050861B

; Patent No. 6555314

; GENERAL INFORMATION:

; APPLICANT: Payan, Donald

; TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING

; FILE REFERENCE: RIGL-002CON

; CURRENT APPLICATION NUMBER: US/09/050,861B

; CURRENT FILING DATE: 1998-03-30

; PRIOR APPLICATION NUMBER: US/09/651,150B

; PRIOR FILING DATE: 2000-08-30

; PRIOR APPLICATION NUMBER: US 09/050,861

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 1911

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-050-861B-1

Query Match 100.0%; Score 1911; DB 4; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1911; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAAGGAGTAAGCAGCGTGTCTCCATGCCCTCTTAGGGCTCTTGGATGGACCTTGCAC	60
Db	1	AAAGGAGTAAGCAGCGTGTCTCCATGCCCTCTTAGGGCTCTTGGATGGACCTTGCAC	60
Qy	61	TCTAGAAGGACAATGGACCTTCTGGCTTTGGCCACTTTACTTCTGCGAGTATCAGGGGC	120
Db	61	TCTAGAAGGACAATGGACCTTCTGGCTTTGGCCACTTTACTTCTGCGAGTATCAGGGGC	120
Qy	121	CCTGAGATCTCCCAAGTAAGGTAGAGGGGAGCTGGCGGATCATGTTACATCAAA	180
Db	121	CCTGAGATCTCCCAAGTAAGGTAGAGGGGAGCTGGCGGATCATGTTACATCAAA	180
Qy	181	ATGCGCACTTCTCAAAATGATGTAGGATATCTGTGGGGAGATGCTGGATCTGG	240
Db	181	ATGCGCACTTCTCAAAATGATGTAGGATATCTGTGGGGAGATGCTGGATCTGG	240
Qy	241	AACATGTGGTACCGTGGTATCCACCACTTTCATCAAGGACAATACAGGGCCGAGT	300
Db	241	AACATGTGGTACCGTGGTATCCACCACTTTCATCAAGGACAATACAGGGCCGAGT	300
Qy	301	TACTTCTGAAGCAATACCCAGCAAGATCTTCTTAGTGAAGTAAACAGCTGACAGA	360
Db	301	TACTTCTGAAGCAATACCCAGCAAGATCTTCTTAGTGAAGTAAACAGCTGACAGA	360

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Db 361 AAGTGACAGCGGAGTCTATGCTTGGGAGGGGGCATGAACACAGACCGGGGAAAGACCCA 420  
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Db 421 GAAAGTCAACCTCAAGTTCACAGTGAATACAGAGCCATCATGGAAGAGCAGCAATGCC 480  
QY 481 TGAGACTCCAAATGTTTTCATCTGCCCTATTTTGTCCAGATGCTCATATGCGCATTC 540  
Db 481 TGAGACTCCAAATGTTTTCATCTGCCCTATTTTGTCCAGATGCTCATATGCGCATTC 540  
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QY 601 CCACTCTCCCGCCACACCAATACCCACCGCTCGAGTGTCCAGAGCATCTTCAGT 660  
Db 601 CCACTCTCCCGCCACACCAATACCCACCGCTCGAGTGTCCAGAGCATCTTCAGT 660  
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Db 841 CCGGACCATCTGGGCTTTTCTGTGGCACTTCTGGGGTGGTGGTGAAGGGCGGT 900  
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QY 1141 TGCCCCATCTCTGAAGACAGCTGTAATAGCTGAGCTCTTACACACAGCGCTGCGGCGAT 1200  
Db 1141 TGCCCCATCTCTGAAGACAGCTGTAATAGCTGAGCTCTTACACACAGCGCTGCGGCGAT 1200  
QY 1201 GATGGAGACAGTATTCAGATGACTACATCAATGTTCTGCGCTGCGACAACTCCCGAGTA 1260  
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QY 1261 TCCGCGCGGAGCGGAGTGTGGTGGCAAGGAGTCTATCTATCTGCTGATGCCA 1320  
Db 1261 TCCGCGCGGAGCGGAGTGTGGTGGCAAGGAGTCTATCTATCTGCTGATGCCA 1320  
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Db 1321 ATACCTGCTCATGTGTTCTCAGAGCCCTCATCACTTCCCATGCGGCTGCGACTGCCA 1380  
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Db 1381 TCCGCGCGGAGCGGAGTGTGGTGGCAAGGAGTGTGGTGGCAAGGAGTGTGGCAAGGAGTGTGG 1440  
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Db 1441 CAGCGCGCTGTGTGACAGTAAAGTGTAGGCGATGAGACCAATGTCGCCAATGCCACT 1500  
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Db 1501 TGCTTCTCTTCCAAAGCCGTCGAACAGACTGTGGGATTTGCAAGTGTTCCTTCCATGTCT 1560  
QY 1561 TTGACACAGAGGTTGTGTGCTGCCAGCTCTAGATCATCATGCGATCAGGCTGGGCGAGA 1620  
Db 1561 TTGACACAGAGGTTGTGTGCTGCCAGCTCTAGATCATCATGCGATCAGGCTGGGCGAGA 1620  
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QY 1681 TTGCTCTGAGTATGTGACGTGCTCGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT 1740  
Db 1681 TTGCTCTGAGTATGTGACGTGCTCGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT 1740  
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QY 1861 CAAGATATGATATATATCCATAATCTCTTTACTCTCTCTCCATCCTTT 1911  
Db 1861 CAAGATATGATATATATCCATAATCTCTTTACTCTCTCTCCATCCTTT 1911

## RESULT 2

US-08-961-564A-1  
; Sequence 1, Application US/08961564A  
; Patent No. 6114515  
; GENERAL INFORMATION:  
; APPLICANT: WU, SHUJIAN  
; APPLICANT: SWEET, RAYMOND  
; APPLICANT: TRUNEH, ALEMSEGED  
; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN  
; TITLE OF INVENTION: GENE SUPERFAMILY  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,564A  
; FILING DATE: 30-OCT-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/056,935  
; FILING DATE: 25-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70236  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2040 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-961-564A-1

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Query Match	96.4%;	Score 1842.4;	DB 3;	Length 2040;
Best Local Similarity	99.2%;	Pred. No. 0;		
Matches 1894; Conservative	0;	Mismatches 11;	Indels 5;	

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QY	65	GAAGGGACAATGACATTCGCTTGGCCACTTACCTTCTGCGCAGTATCAGGGGCCCTG	124								
Db	137	GAAGGGACAATGACATTCGCTTGGCCACTTACCTTCTGCGCAGTATCAGGGGCCCTG	196								
QY	125	AGGATCCTCCAGAAAGTAAAGGTAGAGGGGAGCTGGCGGATCAGTTACATCAAAATGC	184								
Db	197	AGGATCCTCCAGAAAGTAAAGGTAGAGGGGAGCTGGCGGATCAGTTACATCAAGTGC	256								
QY	185	CCACTTCTCGAATGTGAGGATATATCTGTGCCGGAGATGGCTGGATGTGGAACA	244								
Db	257	CCACTTCTCGAATGTGAGGATATATCTGTGCCGGAGATGGCTGGATGTGGAACA	316								
QY	245	TGTGGTACCGTGGTATCCACACCACTTCATCAAGGCAGAAATCAAGGCCCGAGTTACT	304								
Db	317	TGTGGTACCGTGGTATCCACCACTTCATCAAGGCAGAAATCAAGGCCCGAGTTACT	376								
QY	305	CTGAAGCAATPACCCAGCGCAAGAAATCTGTTCCTAGTGGAGGTAAACACAGCTGCAGAAAGT	364								
Db	377	CTGAAGCAATPACCCAGCGCAAGAAATCTGTTCCTAGTGGAGGTAAACACAGCTGCAGAAAGT	436								
QY	365	GACAGGGAGTCTATGCCTCGGAGCGGCATGAACACAGACCAGGGAAGACCCAGAAA	424								
Db	437	GACAGGGAGTCTATGCCTCGGAGCGGCATGAACACAGACCAGGGAAGACCCAGAAA	496								
QY	425	GTCAACCTGAATGCCAGTGAATACGAGCCATCATGGGAAGAGCAGCAATGCCCTGAG	484								
Db	497	GTCAACCTGAATGCCAGTGAATACGAGCCATCATGGGAAGAGCAGCAATGCCCTGAG	556								
QY	485	ACTCCAAAATGGTTTCATCTGGCCTATTTGTTCCAGATGCCTGCATATGCCATTTCTTCC	544								
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QY	545	AAATTCGTACACAGATTACACACAGCTCAAGAGGGCAAGTCCCTCAGTTCACAC	604								
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QY	605	TCTCCGCCACACCCAAATCACCCACCGCCTCGAGTGTCCAGAGCATCTTCAGTAGCA	664								
Db	677	TCTCCGCCACACCCAAATCACCCACCGCCTCGAGTGTCCAGAGCATCTTCAGTAGCA	736								
QY	665	GTGTCAAGCCCCGAACCTTCTGCATCCATACAGCCTCAAAAATCTCAGCTCTGGAG	724								
Db	737	GTGTCAAGCCCCGAACCTTCTGCATCCATACAGCCTCAAAAATCTCAGCTCTGGAG	796								
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QY	785	GCATGGACTATGGCTCAGTCTGGAGGGAGGCAAGGATTTTCACATCTCTGATCCCG	844								
Db	857	GCATGGACTATGGCTCAGTCTGGAGGGAGGCAAGGATTTTCACATCTCTGATCCCG	916								
QY	845	ACCATCTGGGGCTTTTCTGCTGGCACTCTGTGGGCTGGTGGTGAAGGGCCCTTGAA	904								
Db	917	ACCATCTGGGGCTTTTCTGCTGGCACTCTGTGGGCTGGTGGTGAAGGGCCCTTGAA	976								
QY	905	AGGAGGAAGCCCTCTCCAGGCGGCGCCGACCTGGCCGTGAGGATGCGGCCCTTGGAG	964								
Db	977	AGGAGGAAGCCCTCTCCAGGCGGCGCCGACCTGGCCGTGAGGATGCGGCCCTTGGAG	1036								

QY	965	AGCTCCCAAGAGGCCCGCGGGTCGCGCGACGCGGCTCCCCAAAACACATCTACAGCGCC	1024
Db	1037	AGCTCCCAAGAGGCCCGCGGGTCGCGCGACGCGGCTCCCCAAAACACATCTACAGCGCC	1096
QY	1025	TGCGCGCGCGGCTCTGTGGAGCGGACGCTCCAGCACAGGGGAGGCCCGGTTCCCGGC	1084
Db	1097	TGCGCGCGCGGCTCTGTGGAGCGGACGCTCCAGCACAGGGGAGGCCCGGTTCCCGGC	1156
QY	1085	CCGAGAGCCGTTTGCCCGCCCGCCCGCTGCAGGTGTCTGAATCTCCTGSCCTCCATGCC	1144
Db	1157	CCGAGAGCCGTTTGCCCGCCCGCCCGCTGCAGGTGTCTGAATCTCCTGSCCTCCATGCC	1216
QY	1145	CCATCTCTGAGACACAGCTGTGAATAGTGGACCTCTACCACAGCCGTGGCGCAATGATG	1204
Db	1217	CCATCTCTGAGACACAGCTGTGAATAGTGGACCTCTACCACAGCCGTGGCGCAATGATG	1276
QY	1205	GAGGACAGTGAATCAGATGACTACATCAATGTTTCCCTGCCTGACAACTGCCAGTATCCC	1264
Db	1277	GAGGACAGTGAATCAGATGACTACATCAATGTTTCCCTGCCTGACAACTGCCAGTATCCC	1336
QY	1265	CAAACCCAGGCTCGGACTGTGTGTGCCAAGSAGTCTCATCTATCTGCTGATGTCCAATAC	1324
Db	1337	CAAACCCAGGCTCGGACTGTGTGTGCCAAGSAGTCTCATCTATCTGCTGATGTCCAATAC	1396
QY	1325	CTGCTTCATGTGTTCTCAGAGCCCTCATACACTTCCCATGCCCATCTCGACTCCCATCCC	1384
Db	1397	CTGCTTCATGTGTTCTCAGAGCCCTCATACACTTCCCATGCCCATCTCGACTCCCATCCC	1456
QY	1385	CATCTATCTGTGGCCCTGAGCATGGCTGCCCCAGGTGCTCTTGACACACCTTGGCAGC	1444
Db	1457	CATCTATCTGT - GCCCTGAGCATGGCTGCCCCAGGTGCTCTTGACACACCTTGGCAGC	1515
QY	1445	CCCCTGAGTTGACAGGTAAGCTGTAGGCATGTAGAGCAATGTGCCAATGCCACTTGCT	1504
Db	1516	CCCCTGAGTTGACAGGTAAGCTGTAGGCATGTAGAGCAATGTGCCAATGCCACTTGCT	1575
QY	1505	TCCTTTCCAGCCGTGAAACAGACTGTGGGATTTGACAGTGTGTTCTTCATGCTCTTGA	1564
Db	1576	TCCTTTCCAGCCGTGAAACAGACTGTGGGATTTGACAGTGTGTTCTTCATGCTCTTGA	1635
QY	1565	CCAGAGGTTGTGTGCTGCCAGGCTAGATCACATGGCATCAGGTCGGGCGAGAGGA	1624
Db	1636	CCAGAGGTTGTGTGCTGCCAGGCTAGATCACATGGCATCAGGTCGGGCGAGAGGA	1694
QY	1625	TAGCTATTGTCTGGGCAT - CCTTCCAGGGTTGGGTCTTACACAAATGAAGGCTCTTG	1683
Db	1695	TAGCTATTGTCTGGGCATCCCCTCCAGGGTTGGGTCTTACACAAATGAAGGCTCTTG	1754
QY	1684	CTCTGAGTTATGTGACGTGGCTCAGGCCCCATGAGCTAAGCAGGGGTCTGGAT - AAACA	1741
Db	1755	CTCTGAGTTATGTGACATGCTCAGGCCCCATGAGCTAAGCAGGGGTCTGGATATAAACA	1814
QY	1742	CTCCTGAAACGGCTTTGCCCTCATCCAAATGTTGCACTGCTAGTGAACGCTCTACTTA	1801
Db	1815	CTCCTGAAACGGCTTTGCCCTCATCCAAATGTTGCACTGCTAGTGAACGCTCTACTTA	1874
QY	1802	TCTCAAGTTCTATGCTAAAGGCAATTTATCTTGATGTGATGATAAACCAAACTTATTAGC	1861
Db	1875	TCTCAAGTTCTATGCTAAAGGCAATTTATCTTGATGTGATGATAAACCAAACTTATTAGC	1934
QY	1862	AGGATATGCATATATATCCAAATTTCTCTTTACTCTGCTCCATCCCTTT	1911
Db	1935	AGGATATGCATATATATCCAAATTTCTCTTTACTCTGCTCCATCCCTTT	1984

RESULT 3  
US-08-961-564A-3  
; Sequence 3, Application US/08961564A  
; Patent No. 6114515  
; GENERAL INFORMATION:  
; APPLICANT: WO, SHUJIAN  
; APPLICANT: SWEET, RAYMOND

```

; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,564A
; FILING DATE: 30-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,935
; FILING DATE: 25-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-961-564A-3

Query Match 35.4%; Score 676; DB 3; Length 1047;
Best Local Similarity 94.6%; Pred. No. 7.6e-193;
Matches 785; Conservative 0; Mismatches 34; Indels 11; Gaps 8;

QY 5 GAGTAAGCAGCGTCTCCATCCCTCTCTAGGGGCTCTTGGATGGACCTTGACACTA 64
DB 11
DB 81 GAGTAAGCAGCGTCTCCATCCCTCTCTAGGGGCTCTTGGATGGACCTTGACACTA 140
QY 65 GAAGGGACAATGGACTTCTGGCTTGGCCACTTTACTTCTGCGAGTATCAGGGCCCTG 124
DB 141 GAAGGGACAATGGACTTCTGGCTTGGCCACTTTACTTCTGCGAGTATCAGGGCCCTG 200
QY 125 AGGATCTCCAGAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAAAATGC 184
DB 201 AGGATCTCCAGAGTAAGGTAGAGGGGAGCTGGCGGATCAGTTACCATCAAGTGC 260
QY 185 CCAGTTCCTGAAATGCAATGTAAGATATATCTGTCGGGAGATGCGTGGATCGGAACA 244
DB 261 CCAGTTCCTGAAATGCAATGTAAGATATATCTGTCGGGAGATGCGTGGATCGGAACA 320
QY 245 TGTGGTACCGTGTATCCACCACCACTTCATCAAGGCAGATACAGGGCCGAGTTACT 304
DB 321 TGTGGTACCGTGTATCCACCACCACTTCATCAAGGCAGATACAGGGCCGAGTTACT 380
QY 305 CTGAAGCAATACCCACGCAAGAAATCTGTTCTAGTGGAGGTAACACAGCTGCACAGAA 364
DB 381 CTGAAGCAATACCCACGCAAGAAATCTGTTCTAGTGGAGGTAACACAGCTGCACAGAA 440
QY 365 GACAGCGAGTCTATGCTCGGAGCGGGATGAACACAGCCGGGGAAGACCCAGAAA 424
DB 441 GACAGCGAGTCTATGCTCGGGA-CGGGCATGAACACAGCCGGGGAAGACCCAGAAA 499
QY 425 GTCACCCCTGAATGTCACAGTGAATACAGGCCATCATGCGGAGAGACCCCAATGCCTGAG 484

500 GTACACCTGAATGTCACAGTGAATAGAGCCATCAATGGGAAGAGCAGCAATGCCTGAG 559
485 ACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCTCCATATGCCAGTTCTTCC 544
560 ACTCCAAAATGGTTTCATCTGCCCTATTTGTTCCAGATGCTCCATATGCCAGTTCTTCC 619
545 AAATTCGTAAAC--CAGAGTTACACACAGCAGC--TCAAAGGGGAGAGTCCCTCCAGTTAC 601
620 ACATTCGTAAACCGCAGAGTTACACACAGCAGCTTCAAAGGGGAGAGTCCCTCCAGTTAC 679
602 CACTCTCTCCCCACACCCCAAA--TCAGCCACCGCC--TCGAGTGTCCAGAGCATCTTCAG 659
680 CACTCTCTCCCCACACCCCAAAATTCACCCACCGCCCTTCGAGTGTTCAGAGCATCTTCAG 739
660 TAGCAGGTGACAAAGCCCGG--AACTTTCCTGCCATCCACTACAGCTCAAAAATCTCAGCT 718
740 TAGCAGGTGACAAAGCCCGGAAACTTTCCTGCCATCCACTACAGCTCAAAAATCTCAGCT 799
719 CTGGAGGGGCTGCTCAAGCCCC--AGACGCCAGCTACAAACACACACAGCCTGCAC 775
800 CTGGAAGGCTGCTTCAAGCCCCAGAGCCCGCCAGCTACAA--CANACACAGCCTGCAC 858
776 AGCAGAGAGCAGCTGGACTATGGCTCACAGTCTGGGAGGAGGAGGAGGAGG 825
859 AGCAGAGAGCAGCTGGACTATGGCTCACAGTCTGGGAGGAGGAGGAGGAGG 908

RESULT 4
US-09-724-864-11
; Sequence 11 Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Mouse
; US-09-724-864-11

Query Match 29.5%; Score 563.6; DB 4; Length 1480;
Best Local Similarity 67.5%; Pred. No. 5.4e-159;
Matches 940; Conservative 0; Mismatches 389; Indels 63; Gaps 8;

QY 62 CTAGAAGGGACAATGGAGCTTCTGCGCTTTGGCCACTTTACTTCTGCGAGTATCAGGGGCC 121
DB 43 CTCAGGGAACCATGGAGCTTTTGGCTTTGGTTACTTTACTTCTGCGAGTATCAGGGGCC 102
QY 122 CTGAGGATCTCCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTTACCATCAAA 181
DB 103 CTGAGAGCTCTCCAGAGTAAGGTAGAGGGGAGCTGGGGGATCAGTTTATCATCGAA 162
QY 182 TGCCCACTCTGAAATGTCATGTAGGATATATCTGTCGGGAGATGCTGGATCTGGA 241
DB 163 TGCCCACTCTGAAATGTCATGTAGGATATATCTGTCGGGAGATGCTGGATCTGGA 222
QY 242 ACATGTGTACCGTGTATCCACCACCACTTCATCAAGGCAGATACAGGGCCGAGTT 301
DB 223 ATATGCTCCACTGGTGTCCCAACAC---CTTTGTCAAGAGGAATATGAAGGCGAGTTC 279
QY 302 ACTCTGAGAGCAATACCCACGCAAGAAATCTGTTCTAGTGGAGGTAACACAGCTGCAGAA 361
DB 280 ACCCTGAGCGCATGCTTGGATAAAGAGCTATTCCTTAGTGGAGATGACACAGCTGACGAA 339
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QY	362	AGTGACAGCGGAGTCTATGCTGGGAGCGGGCATGAACACAGACCGGGGAAGACCCAG	421
DB	340	AATGACGATGGAATCTATGCTGTTGGTATGAGACAGACAAGGCAAGCCAG	399
QY	422	AAAGTCACCCCTGAATGTCACAGTGAATAC---GAGCCATCATGGGAAGACAGCAATG	478
DB	400	AAATACACCCCTGAATGTCATTAATGAATATCCAGAACCAATCTGGAAGATGAATGGACC	459
QY	479	CTCAGAGATCCAAATGTTTCATCTGCCCTATTGTTCCAGATGCC-----	525
DB	460	TCICGAGCGCCAGATGGTGCACAGATTCTTCGAGCACCAAGATGGCCTGGCTCCACAGGG	519
QY	526	--TGATATGCCAGTTCTTCCAAATTCGTAACCAAGAGTTACCAACACAGCTCAAAAGGGCC	583
DB	520	AGTGAACATCCAGCTCTCTGGAGTCTATAGCCAAAGTTACCAACGCGCGTTCAAAGACT	579
QY	584	AAGTCCCTCCAGTTCACCACTCTCCGCCACCAACCCAAATACACGACCGCCCTCGAGTG	643
DB	580	GAGCCCTCTGGTTCACCGCCCTCCAGCATCACTTCAGTANCCCAACATCCCGAGATT	639
QY	644	TCCAGAGCATCTTCAGTAGCAGGTGCAAGGCCCGGAACCTTCCTGCCATCCACTACAGCC	703
DB	640	TACAGAGCATTTCTGTGTCACTACCAAGTCCCGAGCGTCTCTGCCACCAACCAAGCC	699
QY	704	TCAAAATCTCAGTCTGGAGGGCTGCTCAGGCCCGCAGAGCCCGAGTACAAACACAC	763
DB	700	TCAAGACTTCCACTACAGCAG--CAATCAGGCGCTTAGAGGCCAGCTACAGCCACAC	756
QY	764	ACCAGGCTGCACAGCGCAGAGCAGCTGGACTATGCTCACAGTCTGGAGGGAGGCGCA	823
DB	757	ACCAGACTTCATGACAAAGACACGCCACCATGGCCCACTATGGAGAGAGACCGGA	816
QY	824	GG-----ATTTCATCTGTATCCCGACCATCTCTGGGCGTTTC	862
DB	817	GGGCTTCACATCCCATCCAGAAATTCACATCTGATTCGCACTCTCTGGGCTTCTC	876
QY	863	CTGCTGCACCTCTGGGCGTGGTGCAAGGGCCGTTGAAAGGAGGAAGCCCTCTCC	922
DB	877	TGCTGTTCTTTTGGGACTGGTGTAAGAGAGCCATCAAGAGGAGGAGAGCTCTCC	936
QY	923	AGCGGGCCCGCGACTGSCCGTGAGATGCGGCGCCTGGAGAGCTCC-----	970
DB	937	AGACGTGCGGGCGACTGGCGATGAGGAGCGAGGCGGGGGCTTCCCGCCGCTTCCC	996
QY	971	---CAGAGGCCCGGGTCCGCGGACCGGCTCCCAAACACATCTACAGCGCTGC	1027
DB	997	ACACAGCGCGGATGCCCGCAGAGCGCGCTCCGAGAACACAGCTCTACAGCGCTGC	1056
QY	1028	CCGCGCGCGCTCGTGAGCGGACGCTGCAAGGCACAGGGAGGCGCCCGCTTCCCGGCC	1087
DB	1057	CCCGCGCGCACGGGACACAGAGCTTGGTCCAGCGAGGCTCGCTCTCAAGGCC	1116
QY	1088	GGAGCGCGTTCGCCCGCGCGCTCGAGGTGTGAAATCTCCCTGGCTCCATGCCCA	1147
DB	1117	CCAGCTCAGCTGCCCGCGCTCTCCGCAAGTACTTGAAGCTCTTGGCGCCACACCCCA	1176
QY	1148	TCCTGAAGACCACTGTGAATACGTGAGCTCTACACACAGCTCGCCCATGATGGAG	1207
DB	1177	TCCTCAAGATGACTGTGATACGTGAGCTTGGCTTACCAAGCTGTGTCACACCTGGAA	1236
QY	1208	GACAGTATTCAGATGACTACATCAATGTTCTCTGCTGCAACTCCCGAGCTATCCCCA	1267
DB	1237	GACCCGTATTCAGATGATTACATCAATATTCCTGAC--CCATCTATCTCCCTAGCTATG	1294
QY	1268	ACCCAGGCTCGACTGTGGTGCCAGGAGTCTATCTATCTGCTGATGTCCAAATGCTG	1327
DB	1295	CCCCAGGCCCATCTTCATGCCAATGATCTGCTGTTTGGCTGATGCTCTAGCAGTT	1354
QY	1328	CTTCATGTGTTCTCAGAGCGCT-CATCAGCTTCACATGCCCGCATCTGAGCTCCCATCCCA	1386
DB	1355	TTCCCTTATAGGATCCCTGTGTCAGCGGTATGCTCTATACCTTAAGTGCAGCTCTCACCTGAC	1414

1387 TCTATCTGTGGC 1398  
 I I I I I  
 Db 1415 TATCTGAATGCC 1426  
  
 RESULT 5  
 US-08-232-463-14  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEIFLINGER, F.  
 ; APPLICANT: FALKNER, F. G.  
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Poley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/232,463  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,313  
 ; FILING DATE:  
 ; APPLICATION NUMBER: EP 91 114 300.6  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7218 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; CLONE: pTZgpt-Fls  
 ; US-08-232-463-14

[illegible]





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; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1433 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: Coding Sequence
;     LOCATION: 118...1101
;   OTHER INFORMATION:
;     NAME/KEY: Coding Sequence
;     LOCATION: 118...234
;   OTHER INFORMATION:
;     NAME/KEY: Coding Sequence
;     LOCATION: 235...1101
;   OTHER INFORMATION:
;     PUBLICATION INFORMATION:
;       AUTHORS: Binkert, C., et al.
;       TITLE: Cloning, sequence analysis and expression....
;       JOURNAL: EMBO J.
;       VOLUME: 8
;       ISSUE: 1989
;       PAGES: 2497-2502
;       DATE:
;
; US-09-199-926-1
;
; Query Match      2.2%; Score 41.8; DB 3; Length 1433;
; Best Local Similarity 46.7%; Pred. No. 0.027;
; Matches 133; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
;
; QY 841 CCGAGCATCTGGGCTTTTCCTGCTGGCCTCTTGGGCTGGTGGTGAAGAGGCGGT 900
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 366 CCGAGCAGCTCGGCGCATGCATGGGGCGCTCGGGCCACTCGCGCCACCCCGGGG 307
;
; QY 901 TGAAGAGGAGAAAGCCCTCTCCAGGCGGGCCCGCGACTGGCGTGAGGATGCGGCCCT 960
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 306 CGGCGCAACGGGGGGCGCGCAGCGCGCAGCGCTCGGGTGTGAGGGCGGAGCG 247
;
; QY 961 GGAGAGCTCCAGAGGCCCCGGGTGCGCGGACCGGCTCCCAAAACAACATCTACAG 1020
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 246 GAACAGCCTTCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 187
;
; QY 1021 CGCCTCCCGCGCGCGCTGTGGAGCGACGCTGCAGGCACAGGGGAGCGCCCGCTTC 1080
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 186 CAGCGCAGCAGCGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127
;
; QY 1081 CGGCCCCGAGCGCGCTTGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1125
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 126 CGGCGCATGCTGGCGTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
;
; RESULT 10
; US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-16
;
; Query Match      2.1%; Score 40.8; DB 3; Length 152331;
; Best Local Similarity 47.8%; Pred. No. 0.88;
; Matches 117; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
;
; QY 915 CCCTCTCCAGGCGGGCGGCGGCTGCCAAACACATCTACAGGCGCTGCCCGGCG 974
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 21916 CCGGNGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 21975
;
; QY 975 GGCCCGCGGGTGCAGCGGCGGCTGCCAAACACATCTACAGGCGCTGCCCGGCG 1034
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 21976 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22035
;
; QY 1035 GCGCTGCTGGAGCGGCGGCTGCAGGCACAGGGAGGCGGCGGCGGCGGCGGCGG 1094
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 22036 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22095
;
; QY 1095 CGTTGCGGCGGCGGCGGCGGCTGCAGGTGCTGAAATCTCCCTGGTCCATGCGCCATCTCTGA 1154
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 22096 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 22155
;
; QY 1155 AGACC 1159
;   |||
; Db 22156 CCGCC 22160
;
; RESULT 11
; US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; EARLIER FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
; US-09-368-590-1
;
; Query Match      2.1%; Score 40.6; DB 3; Length 7812;
; Best Local Similarity 50.5%; Pred. No. 0.17;
; Matches 97; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
;
; QY 924 GCGGGGCGGCGGCGGCTGGAGGATGCGGCGGCTGGAGAGTCCCGAGGCGGCGGCG 983
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 1164 GTCATGCGGCGGCGGCGGCTGTCCCGCTGCGGCGGCTGCGGCGGCGGCGGCGGCG 1105
;
; QY 984 GGTGCGGCGGCGGCGGCTGCCAAACACATCTACAGGCGCTGCCCGGCGGCGGCG 1043
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Db 1104 CGCAGCTCCAGGAGAGCGCTCCTGTGTGCGGCGGCGGCGGCTCTCGGCGCTCTCCAGCTCTGTG 1045
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